

Figure 1

SEQ ID NO:1  
Size: 2164  
DNA PKC-ζ,

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1 atgcccagca ggaccgaccc caagatggaa gggagcggcg gccgcgtccg cctcaaggcg
61 cattacgggg gggacatctt catcaccagc gtggacgccg ccacgacctt cgaggagctc
121 tgtgaggaag tgagagacat gtgtcgtctg caccagcagc acccgctcac cctcaagtgg
181 gtggacagcg aaggtgaccc ttgcacggtg tcctcccaga tggagctgga agaggctttc
241 cgcttgcccc gtcagtgcag ggatgaaggc ctcatcattc atgttttccc gagcaccctt
301 gagcagcctg gcctgccatg tccgggagaa gacaaatcta tctaccgccg gggagccaga
361 agatggagga agctgtaccg tgccaacggc caccctcttc aagccaagcg ctttaacagg
421 agagcgtact gcggtcagtg cagcgagagg atatggggcc tcgcgaggca aggctacagg
481 tgcatacaact gcaaaactgct ggtccataag cgctgccacg gcctcgtccc gctgacctgc
541 aggaagcata tggattctgt catgccttcc caagagcctc cagtagacga caagaacgag
601 gacgccgacc ttccttccga ggagacagat ggaattgctt acatttcctc atcccggag
661 catgacagca ttaaagacga ctcgaggagc ctttaagccag ttatcgatgg gatggatgga
721 atcaaaatct ctcaagggct tgggctgcag gactttgacc taatcagagt catcgggcgc
781 gggagctacg ccaaggttct cctggtgcgg ttgaagaaga atgaccaa attacgccatg
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961 cagacgacaa gtcggttgtt cctggtcatt gactacgtca acggcgggga cctgatgttc
1021 cacatgcaga ggcagaggaa gctccctgag gacacgcca ggttctacgc ggccgagatc
1081 tgcatacgccc tcaacttctt gcacgagagg gggatcatct acagggacct gaagctggac
1141 aacgtcctcc tggatgcgga cgggcacatc aagctcacag actacggcat gtgcaaggaa
1201 ggcttgggcc ctggtgacac aacgagcact ttctgcggaa ccccgaaata catcgcccc
1261 gaaatcctgc ggggagagga gtacgggttc agcgtggact ggtgggcgtt gggagtcctc
1321 atgtttgaga tgatggccgg gcgtcccccg ttcgacatca tcaccgacaa cccggacatg
1381 aacacagagg actacctttt ccaagtgtat ctggagaagc ccatccggat ccccggttc
1441 ctgtcgtca aagcctccca tgttttaaaa ggatttttaa ataaggacct caaagagagg
1501 ctcggtgcc ggccacagac tggattttct gacatcaagt cccacgcgtt cttccgcagc
1561 atagactggg acttgctgga gaagaagcag gcgtccctc cattccagcc acagatcaca
1621 gacgactacg gtctggacaa ctttgacaca cagttacca gcgagccgt gcagctgacc
1681 ccagacgatg aggatgccat aaagaggatc gaccagtcag agttcgaagg ctttgagtat
1741 atcaacccat tattgctgtc caccgaggag tcggtgtgag gccgcgtgct tctctgtcgt
1801 ggacacgcgt gattgacctt ttaactgtat ccttaaccac cgcataatga tgccaggctg
1861 ggcacggctc cgagggcgcc cagggacaga cgcttgccgc gagaccgcag agggagagct
1921 cagcgggcgc tgctgggagc agaacagtc ctcacacctg gcccggcagg cagcttcgtg
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2041 gctgtcatgc ggtttccaag gtgcacattt tccacggaaa cagaactcga tgcactgacc
2101 tgctccgcca ggaaagttag cgtgtagcgt cctgaggaat aaaatgttcc gatgaaaaaa
2161 aaaa

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SEQ ID NO:2  
Size: 592  
PRT PKC-ζ

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1 MPSRTDPKME GSGGRVRLKA HYGGDIFITS VDAATTFEEL CEEVRDMCRL HQQHPLTLKW
61 VDSEGDPTV SSQMELEEF RLARQCRDEG LIIHVFPSTP EQGPLPCPGE DKSIIYRRGAR
121 RWRKLYRANG HLFQAKRFNR RAYCGQCSEI IWGLARQGYR CINCKLLVHK RCHGLVPLTC
181 RKHMDSVMP S QEPVDDKNE DADLPSEETD GIAYISSSRK HDSIKDDSED LKPVIDGMDG
241 IKISQGLGLQ DFDLIRVIGR GTYAKVLLVR LKKNDQIYAM KVVKKELVHD DEDIDWVQTE
301 KHVFEQASSN PFLVGLHSCF QTTSRLFLVI EYVNGGDLMF HMQRQRKLPE EHARFYAAEI
361 CIALNFLHER GIIYRDLKLD NVLLDADGHI KLTIDYGMCKE GLPGDITST FCGTPNYIAP
421 EILRGEYGF SVDWWALGVL MFEMMAGRSP FDIITDNPDM NTEDYLFQVI LEKPIRIPRF
481 LSVKASHVLK GFLNKDPKER LGCRPQTGFS DIKSHAFRFS IDWDLLEKKQ ALPPFPQKIT
541 DDYGLDNFDT QFTSEPVQLT PDDEDAIKRI DQSEFEGFEY INPLLLSTEE SV

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Figure 2  
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SEQ ID NO: 3  
Size: 3663  
DNA PLC-β1

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121 ccaattatth tgaggactga cctcagggg ttttctttt actggacaga tcaaaacaag
181 gagacagagc tactggatct cagccttgtc aaagatgcca gatgtgggag acacgccaaa
241 gctcccaagg accccaaatt acgtgaactt ttggatgtgg ggaacatcgg gcgcctggag
301 cagcgcatga tcacagtggg gtatgggcct gacctcgtga acatctccca tttgaatctc
361 gtggctttcc aagaagaagt ggccaaggaa tggacaaatg aggttttcag tttggcaaca
421 aacctgctgg cccaaaacat gtccagggat gcatttctgg aaaaagccta tactaaactt
481 aagctgcaag tcaactccaga agggcggtatt cctctcaaaa acatatatcg cttgttttca
541 gcagatcgga agcgagtga aactgcttta gaggttgta gtcttccatc ttcaaggaat
601 gattcaatac ctcaagaaga ttctactcca gaagtgtaca gagttttcct caacaacctt
661 tgccctcgac ctgaaattga taacatcttt tcagaatttg gtgcaaaaag caaaccatat
721 cttaccgttg atcagatgat ggattttatc aaccttaagc agcgagatcc tgggcttaat
781 gaaatacttt atccacctct aaaacaagag caagtccaag tattgattga gaagtatgaa
841 ccaacaaca gcctcgccag aaaaggacaa atatcagtgg atgggttcac gcgctatctg
901 agtgagaaag aaaacggagt cgtttcacct gagaaactgg atttgaatga agacatgtct
961 cagccccctt ctactattt cattaattcc tcgcacaaca cctacctcac agctggccaa
1021 ctggctggaa actcctctgt tgagatgtat cgccaagtgc tctgtctgg ttgtcgtgt
1081 gtggagctgg actgctggaa gggacggact gcagaagagg aacctgtcat caccatggc
1141 ttcaccatga caactgaaat atctttcaag gaagtgatag aagcaattgc ggagtgtgca
1201 ttaagactt caccttttcc aattctcctt tcgtttgaga accatgtgga ttcccaaaag
1261 cagcaagcca agatggcgga gtactgccga ctgatctttg gggatgcctt tctcatggag
1321 cccttgaaa aatatccact ggaatctgga gttcctcttc caagccctat ggatttaatg
1381 tataaaatth tggtgaaaaa taagaagaaa tcacacaagt catcagaagg aagcggcaaa
1441 aagaagctct cagaacaagc ctccaacacc tacagtgact cctccagcat gttcgagccc
1501 tcatccccag gagccggaga agctgatacg gaaagtgacg acgacgatga tgatgatgac
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1621 atgtctaatc tggtgaaacta tattcagcca gtcaagtttg agtcatttga aatttcaaaa
1681 aaaagaaata aaagtthtga aatgtcttcc ttcgtggaaa ccaaggact tgaacaactc
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2281 cgtatcttgc cagtgaagc cattcgccca ggctatcact atatctgtct aaggaatgaa
2341 aggaaccagc ctctgacgct gcctgctgtc tttgtctaca tagaagtgaag agactatgtg
2401 ccagacacat atgcagatgt catcgaagct ttatcaaaac caatccgata tgtgaacctg
2461 atggaacaga gagctaagca attggctgct ttgacactgg aagatgaaga agaagtaaag
2521 aaagaggctg atcctggaga aacaccatca gaggtccaa gtgaagcgag aacgactcca
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2641 cacagccagc cagctccagg ttctgtaaag gcacctgcca aaacagaaga tcttatcag
2701 agtgtcttaa cagaagtgga agcacagacc atcgaagaac taaagcaaca gaaatcgtht
2761 gtgaaacttc aaaagaaaca ctacaaagaa atgaaagacc tggtaagag acaccacaag
2821 aaaaccactg accttatcaa agaacacact accaagtata atgaaattca atgactac
2881 ttgagaagga gagccgcttt ggaaaagtcc gccaaaaagg acagtaagaa aaaatcgga
2941 ccagcagcc ctgatcatgg ttcacacagc attgagcaag acctcgctgc tctggatgct
3001 gaaatgaccc aaaagttaat agacttgaag gacaaacaac agcagcagct gcttaatctt
3061 cggcaagaac agtattatag tgaaaaatc cagaagcgag aacatattaa actgcttatt
3121 caaaagttga cggatgtcgc agaagagtgt cagaacaatc agttaagaa gctcaagaa
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Figure 2  
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3181 atctgtgaga aagaaaagaa agaattaaag aagaaaatgg ataaaaagag gcaggagaag
3241 ataacagaag ctaaatacaa agacaaaagt cagatggaag aggagaagac agagatgatk
3301 cggtcataata tccaggaagt ggtgcagtat atcaagaggc tagaagaagc gcaaagtaaa
3361 cggcaagaaa aactcgtaga gaaacacaag gaaatacgtc agcagatcct ggatgaaaag
3421 cccaagctgc aggtggagct ggagcaagaa taccaagaca aattcaaaaag actgcccctc
3481 gagatttttg aattcgtaga ggaagccatg aaaggaaaaga tcagtgaaga cagcaatcac
3541 ggttctgccc ctctctccct gtcctcagac cctggaaaag tgaaccacaa gactccctcc
3601 agtgaggagc tgggaggaga catcccagga aaagaatttg atactcctct gtgaatgctc
3661 ctg

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SEQ ID NO:4

Size: 1216

PRT PLC-β1

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1  MAGAQPGVHA LQLKPVCVSD SLKKGTKFVK WDDSTIVTP IILRTDPQGF FFYWTDQNK
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121 AFQEEVAKW TNEVFSLATN LLAQNMSRDA FLEKAYTKLK LQVTPGGRIP LKNIYRLFSA
181 DRKRVETALE ACSLPSSRND SIPQEDFTPE VYRVFLNNLC PRPEIDNIFS EFGAKSKPYL
241 TVDQMMDFIN LKQRPRLNE ILYPPLKQEQ VQVLEIKYEP NNSLARKGQI SVDGFMRYLS
301 GEENGVSPE KLDLNEDEMSQ PLSHYFINSS HNTYLTAGQL AGNSSVEMYR QVLLSGCRCV
361 ELDCWKGRTA EEEPVITHGF TMTTEISFKE VIEAIAECAF KTSPPFILLS FENHVDSPKQ
421 QAKMAEYCRL IFGDALLMEP LEKYPLESGV PLPSPMDLMY KILVKNKKKS HKSSESGGKK
481 KLSEQASNTY SDSSSMFEPS SPGAGEADTE SDDDDDDDDDC KKSSMDEGTA GSEAMATEEM
541 SNLVNYIQPV KFESFEISK RNKSFEMSSF VETKGLEQLT KSPVEFVEYN KMQLSRIYPK
601 GTRVDSSNYM PQLFWNAGCQ MVALNFQTM LAMQINMGMY EYNGKSGYRL KPEFMRRPDK
661 HFDPFTEGIV DGIVANTLSV KIISGQFLSD KKVGTVEVD MFGLPVDTRR KAFKTKTSQG
721 NAVNPWEEE PIVFKKVLP TLACLRIVY EEGGKFIGHR ILPVQAIRPG YHYICLRNER
781 NQPLTLPAVF VYIEVKDYVP DTYADVIEAL SNPIRYVNL EQRKQLAAL TLEDEEEVKK
841 EADPGETPSE APSEARTTPA ENGVNHTTTL TPKPPSQALH SQPAPGSVKA PAKTEDLIQS
901 VLTEVEAQTI EELKQKSFV KLQKKHYKEM KDLVKRHHKK TTDLIKEHTT KYNEIQNDYL
961 RRAALEKSA KKDSKKKSEP SSPDHGSSTI EQDLAALDAE MTQKLIDLKD KQQQQLNLN
1021 QEQQYSEKYQ KREHIKLLIQ KLTDAEECQ NNQLKKLKEI CEKEKKELKK KMDKKRQEKI
1081 TEAKSKDKSQ MEEKTEKEMIR SYIQEVVQYI KRLEEAQSKR QEKLVEKHKE IRQQILDEKP
1141 KLQVELEQY QDKFKRLPLE ILEFVQEAMK GKISEDNSHG SAPLSLSSDP GKVNHKTPSS
1201 EELGGDIPGK EFDTP

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Figure 3  
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SEQ ID NO:5  
Size: 3052  
DNA FAK

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1  ccggtgtgaa  ggccatgagt  gattactggg  ttgttggaaa  gaagtctaac  tatgaagtat
61  tagaaaaaga  tgttggttta  aagcgatttt  ttcctaagag  tttactggat  tctgtcaagg
121  ccaaaacact  aagaaaactg  atccaacaaa  catttagaca  atttgccaac  cttaatagag
181  aagaaagtat  tctgaaattc  tttgagatcc  tgtctccagt  ctacagattt  gataaggaat
241  gcttcaagtg  tgctcttggg  tcaagctgga  ttatttcagt  ggaactggca  atcggcccgag
301  aagaaggaat  cagttaccta  acggacaagg  gctgcaatcc  cacacatctt  gctgacttca
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961  ccaggaatgc  agagttaaca  atgcgtcagt  ttgaccatcc  tcatattgtg  aagctgattg
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1801  ctgggtcaca  tggaaatcaca  gccatggctg  gcagcatcta  tccaggtcag  gcatctcttt
1861  tggagccaac  agattcatgg  aatcatagat  ctccaggagat  agcaatgtgg  agccccaatg
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1981  tgggaagagc  tctaatacga  cagcaacagg  aaatggaaga  agatcagcgc  tggctggaaa
2041  aagaggaaag  atttctgatt  ggaaaccaac  atatatatca  gcctgtgggt  aaaccagatc
2101  ctgcagctcc  accaaagaaa  ccgcctcgcc  ctggagctcc  cggctcatctg  ggaagccttg
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2401  atgagaccat  tcccctccta  ccagccagca  cccaccgaga  gattgagatg  gcacagaagc
2461  tattgaactc  tgacctgggt  gagctcatca  acaagatgaa  actggcccag  cagtatgtca
2521  tgaccagcct  ccagcaagag  taaaaaaagc  aaatgctgac  tgccgctcac  gccctggctg
2581  tggatgccaa  aaacttactc  gatgtcattg  accaagcaag  actgaaaatg  cttgggcaga
2641  cgagaccaca  ctgagcctcc  cctaggagca  cgtcttgcta  cctcttttg  aagatgttct
2701  ctagccttcc  accagcagcg  aggaattaac  cctgtgtcct  cagtccgag  cactcacagc
2761  tccaactttt  ttgaatgacc  atctggttga  aaaatctttc  tcatataagt  ttaaccacac
2821  tttgatttgg  gttcattttt  tgttttgtt  ttttcaatca  tgatattcag  aaaaatccag
2881  gatccaaaat  gtggcgtttt  tctaagaatg  aaaattatat  gtaagctttt  aagcatcatg
2941  aagaacaatt  tatgttcaca  ttaagatacg  ttctaagggt  ggaatggcaa  ggggtgacat
3001  cttaattcct  aaactacctt  agctgcatag  tggaaagagga  gagccggaat  tc
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Figure 3  
Page 2 of 2

SEQ ID NO:6  
Size: 879  
PRT FAK

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1  MSDYWVVGKK SNYEVLKDV GLKRFFPKSL LDSVKAKTLR KLIQQTFRQF ANLNREESIL
61  KFFEILSPVY RFDKECFKCA LGSSWIISVE LAIGPEEGIS YLTDKGCNPT HLAFTQVQT
121 IQYSNSEDKD RKGMLQLKIA GAPEPLTVTA PSLTIAENMA DLIDGYCRLV NGTSQSFIIR
181 PQKEGERALP SIPKLANSEK QGMRTHAVSV SETDDYAEII DEEDTYTMPs TRDYEIQRER
241 IELGRCIGEG QFGDVHQGIY MSPENPALAV AIKTCKNCTS DSVREKFLQE ACHYTSLHWN
301 WCRYISDPNV DACPDPRNAE LTMRFQDHPH IVKLIGVITE NPVWIIMELC TLGELRSFLQ
361 VRKYSLDLAS LILYAYQLST ALAYLESKRF VHRDIAARNV LVSSNDCVKL GDFGLSRYME
421 DSTYYKASKG KLPIKWMAPE SINFRRFTSA SDVWMFGVCM WEILMHGVKP FQGVKNNDVI
481 GRIENGERLP MPPNCPPTLY SLMTKCWAYD PSRRPRFTEL KAQLSTILEE EKAQQEERMR
541 MESRRQATVS WDSGGSDEAP PKPSRPGYPS PRSSEGFYPS PQHMQVTNHY QVSGYPGSHG
601 ITAMAGSIYP GQASLLDQTD SWNHRSQEIA MWQPNVEDST VLDLRGIGQV LPTHLMEERL
661 IRQQQEMEED QRWLEKEERF LIGNQHIYQP VGKPDPAAPP KKPPRPGAPG HLGSLASLSS
721 PADSYNIEGVK LQPQEISPPP TANLDRSNDK VYENVTLGLVK AVIEMSSKIQ PAPPEEYVPM
781 VKEVGLALRT LLATVDETIP LLPASTHREI EMAQKLLNSD LGELINKMKL AQQYVMTSLQ
841 QEYKKQMLTA AHALAVIDAKN LLDVIDQARL KMLGQTRPH
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Figure 4  
Page 1 of 2

SEQ ID NO:7  
Size: 4089  
DNA FAK2

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1 gaattccgtc agccctttta ctcagccaca gcctccggag ccgttgacaca cctacctgcc
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121 cgctggagtc cgcgcctccc tgggactgca atgtgccgat cttagctgct gcctgagagg
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241 ggccctgcag agcccatggt ggtggtacca gtagatgtgg aaaaggagga cgtgcgtatc
301 ctcaaggtct gcttctatag caacagcttc aatcctggga aaaacttcaa actggtcaaa
361 tgcactgtcc agacggagat ccgggagatc atcacctcca tccgtctgag cgggcggatc
421 gggcccaaca tccggttggc tgagtgttat gggctgaggc tgaagcacat gaagtcgat
481 gagatccact ggctgcaccc acagatgacg gtgggtgagg tgcaggacaa gtatgagtgt
541 ctgcacgtgg aagccgagtg gaggtatgac cttcaaattc gctacttgcc agaagacttc
601 atggagagcc tgaaggagga caggaccacg ctgctctatt ttaccaaca gctccggaac
661 gactacatgc agcgtacgc cagcaaggtc agcaggggca tggccctgca gctgggctgc
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781 ttcgagctcc tagaaaagga agtggggctg gacttgtttt tcccaaagca gatgcaggag
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961 gaccaggaga cctaccgctg tgaactcatt caaggatgga acattactgt ggacctggtc
1021 attggcccta aagggatccg ccagctgact agtcaggacg caaagccac ctgcctggcc
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1141 cagctgggca ttgaaggtgc cccccaggcc ttgtccatca aaacctcatc cctagcagag
1201 gctgagaaca tggctgacct catagacggc tactgccggc tgcagggtga gcaccaaggc
1261 tctctcatca tccatcctag gaaagatggt gagaagcggg acagcctgcc ccagatcccc
1321 atgctaaacc tggaggcccg gcggtccac ctctcagaga gctgcagcat agactcagac
1381 atctacgcag agattcccg cgaaacctg cgaaggcccg gaggtccaca gtatggcatt
1441 gcccggtgaag atgtggtcct gaatcgtatt cttggggaag gcttttttgg ggaggtctat
1501 gaaggtgtct acacaaatca taaaggggag aaaaatcaatg tagctgtcaa gacctgcaag
1561 aaagactgca ctctggacaa caaggagaag ttcatgagcg aggcagtgat catgaagaac
1621 ctgcaccacc cgcacatcgt gaagctgatc ggcatcattg aagaggagcc cacctggatc
1681 atcatggaat tgtatcccta tggggagctg ggccactacc tggagcggaa caagaactcc
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1861 gagtgtgtga agctggggga ctttggctct tcccgttaca ttgaggacga ggactattac
1921 aaagcctctg tgactcgtct ccccatcaaa tggatgtccc cagagtccat taacttccga
1981 cgcttcacga cagccagtga cgtctggatg ttccgctgtg gcatgtggga gatcctgagc
2041 tttgggaagc agcccttctt ctggctggag aacaaggatg tcatcggggg gctggagaaa
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2161 tgctgggact acgaccccg tgaccggccc cgcttcaccg agctgggtgt cagcctcagt
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2281 acccccaaaa tcttggagcc cacagccttc caggaacccc cacccaagcc cagccgacct
2341 aagtacagac cccctccgca aaccaacctc ctggctccaa agctgcagtt ccaggttcct
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2461 aactcactgc acacccacc tctccaccgg cacaatgtct tcaaacgcca cagcatgggg
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2761 aggtcgggcg cacagtccat ccagccaca gctaacctgg accggaccga tgacctggtg
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2881 ctgccccccg agggctacgt ggtggtggtg aagaatgtgg ggctgacctc gcggaagctc
2941 atcggggagcg tggatgatct cctgccttcc ttgccgtcat cttcacggac agagatcgag
3001 ggcacccaga aactgctcaa caaagacctg gcagagctca tcaacaagat gcggctggcg
3061 cagcagaacg ccgtgacctc cctgagtgag gagtgaaga ggcagatgct gacggcttca
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3181 gccaatctgg cccacccacc tgcagagtga cggagggtgg gggccacctg cctgcgtctt
3241 ccgccccctg ctgccatgta cctcccctgc cttgctgttg gtcagtgtgg tcttccaggg
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Figure 4  
Page 2 of 2

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3301 agaaggccaa ggggagtcac cttcccttgc cactttgcac gacgccctct cccacccct
3361 acccctggct gtactgctca ggctgcagct ggacagaggg gactctgggc tatggacaca
3421 ggggtgacggt gacaaagatg gctcagaggg ggactgctgc tgccctggcca ctgctcccta
3481 agccagcctg gtccatgcag ggggctcctg ggggtgggga ggtgtcacat ggtgcccta
3541 gctttatata tggacatggc aggccgattt ggggaaccaag ctattccttt ccttcctct
3601 tctccctca gatgtccctt gatgcacaga gaagctgggg aggagctttg ttttcggggg
3661 tcaggcagcc agtgagatga gggatgggcc tggcattctt gtacagtgtg tattgaaatt
3721 tatttaatgt gaggtttggt ctggactgac agcatgtgcc ctctgaggg aggaccaggg
3781 cacagtccag gaacaagcta attgggagtc caggcacagg atgctgtgtt gtcaacaac
3841 caagcatcag ggggaagaag cagagagatg cggccaagat aggaccttg gccaaatccg
3901 ctctcttctt gcccctcttt ctctttcttc ctttactttt ccttgctttt cctctttttc
3961 ttactcctcc tctttctctc cccaccccc attctcatct gcaccttct tttctcatgt
4021 gtttgcataa acattctttt aacttctttc tatttgactt gtggttgaat taaaattgtc
4081 ccatttgca
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SEQ ID NO:8  
Size: 1009  
PRT FAK2

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1 MSGVSEPLSR VKLGTLLRPE GPAEPMVVVP VDVEKEDVRI LKVCFYNSNF NPGKNFKLVK
61 CTVQTEIREI ITSILLSGRI GPNIRLAECY GLRLKHKMSD EIHWHLPQMT VGEVQDKYEC
121 LHVEAEWRYD LQIRYLPEDF MESLKEDRTT LLYFYQQLRN DYMORYASKV SEGMAQLGQC
181 LELRRFFKDM PHNALDKKSN FELLEKEVGL DLFFPKQMQE NLKPKQFRKM IQQTFQQYAS
241 LREEECVMKF FNTLAGFANI DQETYRCALI QGWNITVDLV IGPKGIRQLT SQDAKPTCLA
301 EFKQIRSIRC LPLEEGQAVL QLGIEGAPQA LSIKTSSLAE AENMADLIDG YCRLQGEHQG
361 SLIIHPRKDG EKRNSLPQIP MLNLEARSH LSESCSIESD IYAEIPDETL RRPGGPQYGI
421 AREDVVLNRI LGEGFFGEVY EGVYTNHKG KINVAVKTC KDCTLDNKEK FMSEAVIMKN
481 LDHPHIVKLI GIIEEPTWI IMELYPYGE GHYLERKNKS LKVLTLVLYS LQICKAMAYL
541 ESINCVHRDI AVRNLVSP ECVKLGDFGL SRYIEDEDY KASVTRLPIK WMSPEINFR
601 RFTTASDVWM FAVCMWEILS FGKQPFWLE NKDVIGVLEK GDRLPKPDLC PPVLYTLMTR
661 CWDYDPSDRP RFTELVCSL DVYQMEKDIA MEQERNARYR TPKILEPTAF QEPKPSRP
721 KYRPPQTNL LAPKLQFQVP EGLCASSPTL TSPMEYPSPV NSLHTPPLHR HNVFKRHSR
781 EEDFIQSSR EEAQQLWEAE KVKMRQILDK QKQMVEDYQ WLRQEEKSLD PMVYMNDKSP
841 LTPEKEVGYL EFTGPPQKPP RLGAQSIQPT ANLDRDLDL YLNMELVRA VLELKNELCQ
901 LPPEGYVVVV KNVGLTLRKL IGSVDDLPS LPSSSRTEIE GTQKLLNKDL AELINKMRLA
961 QQNAVTSLS ECKRQMLTAS HTLAVDAKNL LDAVDQAKVL ANLAHPPAE
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Figure 5

SEQ ID NO:9  
Size: 2195  
DNA CK2

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1 aggggagagc ggccgcccgc gctgccgctt ccaccacagt ttgaagaaaa caggtctgaa
61 acaaggtctt acccccagct gcttctgaac acagtgactg ccagatctcc aaacatcaag
121 tccagctttg tccgccaacc tgtctgacat gtcgggaccc gtgccaaagca gggccagagt
181 ttacacagat gttaatacac acagacctcg agaatactgg gattacgagt cacatgtggt
241 ggaatgggga aatcaagatg actaccagct gggtcgaaaa ttaggccgag gtaaatacag
301 tgaagtattt gaagccatca acatcacaaa taatgaaaaa gttgttgtaa aaattctcaa
361 gccagtaaaa aagaagaaaa ttaagcgtga aataaagatt ttggagaatt tgagaggagg
421 tcccaacatc atcacactgg cagacattgt aaaagaccct gtgtcacgaa cccccgcctt
481 ggtttttgaa cacgtaaaca acacagactt caagcaattg taccagacgt taacagacta
541 tgatattcga ttttacatgt atgagattct gaaggccctg gattattgtc acagcatggg
601 aattatgcac agagatgtca agccccataa tgtcatgatt gatcatgagc acagaaagct
661 acgactaata gactgggggt tggctgagtt ttatcatcct ggccaagaat ataatgtccg
721 agttgcttcc cgatacttca aaggtcctga gctacttgta gactatcaga tgtacgatta
781 tagtttggtt atgtggagtt tgggttggtat gctggcaagt atgatcttcc ggaaggagcc
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901 agaagattta tatgactata ttgacaaata caacattgaa ttatgatccac gtttcaatga
961 tatcttgggc agacactctc gaaagcgatg ggaacgcttt gtccacagtg aaaatcagca
1021 ccttgctcagc cctgaggcct tggatttcct ggacaaaactg ctgcatatg accaccagtc
1081 acggcttact gcaagagagg caatggagca cccctatttc tacactgttg tgaaggacca
1141 ggctcgaatg ggttcacta gcatgccagg gggcagtagc cccgtcagca gcgccaatat
1201 gatgtcaggg atttcttcag tgccaacccc ttcaccctt ggacctctgg caggctcacc
1261 agtgattgct gctgccaacc ccttgggat gcctgttcca gctgccgctg gcgctcagca
1321 gtaacggccc tatctgtctc ctgatgcctg agcagaggtg ggggagtgca cctctcctt
1381 gatgcagctt gcgcctggcg gggaggggtg aaacacttca gaagcaccgt gtctgaaccg
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1501 tttttctttt tttttttaac tcgaactttt cataactcag gggattccct gaaaaattac
1561 ctgcaggtgg aatatttcat ggacaaaatt ttttttctcc cctcccaaat ttagttcctc
1621 atcacaaaaa aacaaaagata aaccagcctc aatcccggct gctgcattta ggtggagact
1681 tcttccattt cccaccattg ttctccacc gtccacact ttagggggtt ggtatctcgt
1741 gctcttctcc agagattaca aaaatgtagc ttctcagggg aggcaggaaag aaaggaagga
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1861 catcacttta ctccataagc gcttcagtg ggttatccta gtggctcttg tggagtggtg
1921 tcttagttac atcaagatgt tgaaaatcta cccaaaatgc agacagatac taaaaacttc
1981 tggttcagtaa gaatcatgtc ttactgatct aaccctaaat ccaactcatt tatactttta
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SEQ ID NO:10  
Size: 391  
PRT CK2

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1 MSGPVPSPRAR VYTDVNTHRP REYWDYESHV VEWGNQDDYQ LVRKLGRGKY SEVF EAINIT
61 NNEKVVVKIL KPVKKKKIKR EIKILENLRG GPNIITLADI VKDPVSRTPA LVFEHVNNTD
121 FKQLYQTLTD YDIRFYMYEI LKALDYCHSM GIMHRDVKPH NVMIDHEHRK LRLIDWGLAE
181 FYHPGQEYNV RVASRYFKGP ELLVDYQMYD YSLDMWSLGC MLASMI FRKE PFFHGH DNYD
241 QLVRIAKVLG TEDLYDYIDK YNIELDPRFN DILGRHSRKR WERFVHSENQ HLVSP EALDF
301 LDKLLRYDHQ SRLTAREAME HPYFYTVVKD QARMGSSSMP GGSTPVSSAN MMSGISSVPT
361 PSPLGPLAGS PVIAAANPLG MPVPAAGAGQ Q

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Figure 6  
Page 1 of 2

SEQ ID NO:11  
Size: 4626  
DNA cMET

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121  cggagcgcgc  gtgtggtect  tgcgcgcgtg  acttctccac  tggttcctgg  gcaccgaaag
181  ataaacctct  cataatgaag  gccccgcgtg  tgcttgacc  tggcatcttc  gtgctcctgt
241  ttaccttggg  gcagaggagc  aatggggagt  gtaaagaggc  actagcaaag  tccgagatga
301  atgtgaatat  gaagtatcag  cttcccaact  tcaccgcgga  aacacccatc  cagaatgtca
361  ttctacatga  gcatcacatt  ttcttgggtg  ccactaacta  catttatgtt  ttaaattgag
421  aagaccttca  gaaggttgct  gagtacaaga  ctgggcctgt  gctggaacac  ccagattgtt
481  tcccatgtca  ggactgcagc  agcaaagcca  atttatcagg  aggtgtttgg  aaagataaca
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2281  catgtacttt  aaaaagtgtg  tcaaacagta  ttcttgaatg  ttatacccca  gcccaaacca
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2521  gcacaataac  aggtgttggg  aaaaacctga  attcagttag  tgtcccgaga  atggtcataa
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3121  gaaagcaaat  taaagatctg  ggcagtgaat  tagttcgcta  cgatgcaaga  gtacacactc
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Figure 6  
Page 2 of 2

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3181 ctcattttgga taggcttgta agtgcccga ggtgaagccc aactacagaa atgggtttcaa
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4141 aagggagaag actcctacaa cccgaatact gcccagacc cttatatgaa gtaatgctaa
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4261 cagcgatctt ctctactttc attggggagc actatgtcca tgtgaacgct acttatgtga
4321 acgtaaaatg tgtcgtccg tatecttctc tgttgtcatc agaagataac gctgatgatg
4381 aggtggacac acgaccagc tcttctggtg agacatcata gtgctagtac tatgtcaaag
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4501 attctttgct ccttgccata ggacttgtat tgttatttaa attactggat tctaaggaat
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4621 ctgcag
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SEQ ID NO:12  
Size: 1408  
PRT cMET

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1 MKAPAVLAPG ILVLLFTLVQ RSNGECKEAL AKSEMNVNMK YQLPNFTAET PIQNVILHEH
61 HIFLGATNYI YVLNEEDLQK VAEYKTGPVL EHPDCFPQCD CSSKANLSSG VWKDNINMAL
121 VVDITYDDQL ISCGSVNRGT CQRHVFPNH TADIQSEVHC IFSPQIEEPS QCPDCVVSAL
181 GAKVLSSVKD RFINFFVGNT INSSYFPDHP LHSISVRLK ETKDGMFLT DQSYIDVLPE
241 FRDSYPIKYV HAFESNNFIY FLTVQRETL AQTFHTRIIR FCSINSLHS YMEMPLECIL
301 TEKRKRSTK KEVFNILQAA YVSKPGAQLA RQIGASLND ILFGVFAQSK PDSAEPMDRS
361 AMCAFKIKYV NDFFNKIVNK NNVRCLQHFY GPNHEHCFNR TLLRNSSGCE ARRDEYRTEF
421 TTALQRVDLF MGQFSEVLLT SISTFIKGD L TIANLGTSEG RFMQVVVSRS GPSTPHVNFL
481 LDSPVSPPEV IVEHTLNQNG YTLVITGKKI TKIPLNGLGC RHFQSCSQCL SAPPFVQCGW
541 CHDKCVRSEE CLSGTWTQOI CLPAIYKVFP NSAPLEGGR LTICGWDFGF RRNNKFDLKK
601 TRVLLGNESC TLTLSESTMN TLKCTVGPAM NKHFNMSSII SNGHGTQYS TFSYVDPVIT
661 SISPKYGPMA GGTLLTLTGN YLNSGNSRHI SIGGKTCTLK SVSNSILECY TPAQTISTEF
721 AVKLKIDLAN RETSIFSIRE DPIVYEIHPT KSFISTWKE PLNIVSFLFC FASGGSTITG
781 VGKNLNSVSV PRMVINVHEA GRNFTVACQH RSNSEIICCT TPSLQQLNLQ LPLKTKAFFM
841 LDGILSKYFD LIYVHNPFVK PFEKPMISM GNENVLEIKG NDIDPEAVKG EVLKVGNKSC
901 ENIHLHSEAV LCTVPNDLLK LNSELNIEWK QAISSTVLGK VIVQPDQNF GLIAGVVSIS
961 TALLLLLGFF LWLKKRKQIK DLGSELVRYD ARVHTPHLDR LVSARSVSPT TEMVSNESVD
1021 YRATFPEDQF PNSSQNGSCR QVQYPLTDM PILTSGDSI SSPLLQNTVH IDLSALNP EL
1081 VQAVQHVVIG PSSLIVHFNE VIGRGHFGCV YHGTLLDNDG KKIHC AVKSL NRITDIGEVS
1141 QFLTEGIIMK DFSHPNVL SL LGICLRSEGS PLVVL PYMKH GD LRNFIRNE THNP TVKDLI
1201 GFGLQVAKAM KYLASKKFVH RDLAARN CML DEKFTVKVAD FGLARDMYDK EYYSVHNKTG
1261 AKLPVKWMAL ESLQTQKFTT KSDVWSFGVV LWELMTRGAP PYPDVNTFDI TVYLLQGRRL
1321 LQPEYCPDPL YEVM LK C WHP KAEMRPSFSE LVS RISAIFS TFI GEHYVHV NATYVNVKCV
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Figure 7  
Page 1 of 2

SEQ ID NO:13  
Size: 3350  
DNA FEN1

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1  cacagtccac tctgtcaggg tttaaggcag gaaaaacatg ctcatTTtga tggtaatat
61  cttccttctc aacattccat ttctcctggc aaatttcatg gatcccagat gcttttgga
121 aataaatTTg aatgaaatca aggatgaagt ccttgggatg acttgTtct tcatccttga
181 aacagttcag aagactatgg acaaagatta tttcaaccag actctgaatg tcctaaatac
241 aactacaaac cacaatatg ccttggcatt ggcttttaca gtggatgaaa tcaacaggaa
301 tcctgatctt ttaccaaata tgtctctgat tataaaatac aatttgggtc atttgtatgg
361 aaaaactgta acaactctat ccgatttatt taatccaaat aatcatctcc atttcccaa
421 ttatttatgt aatgaaggga ttatgtgttt ggttctgctt acaggaccac attggagagc
481 atctttatat ctctggatat ccgtgtatgt ctacctgtct ccacatttcc ttcagctttc
541 ctatggacct ttctactcca tcttcagtga taatgaacaa tatccttate tcatcagat
601 gggcccaaag gactcatcac tagcattggc aatgggtctc ttcataatTT acttcaagt
661 gaactgggtt gggctatttt tctcagatga tgatcaaggc aatcaatttc tctcagagt
721 gaaaaaagag agccaaacca aggatatttt ctttgccttt gtgaacatga tatcagtcag
781 tgatgtttca tactatcata aaactgaaat gtactacaac caaattgtga tgtcatccac
841 aaaggttatt atcatttatg gggaaacaaa cagtattatt gaattgagct tcagaatgtg
901 gtcactctca gttaaacaga gaatatgggt caccacaaaa caatttgatt gccctaccag
961 taagagagac ttaactcatg gcacattcta tgggacctt acatttctac accactatgg
1021 tgagatttct ggcttttaaaa attttgtaca gacacggtac aatctcagaa gcacagattt
1081 atatctagta atgccagagt ggaaatattt taactatgaa gcctcagcat ctaactgtaa
1141 aatactgaga aactattttat ccaatatctc actggaatgg ctaatggaac agaaatttga
1201 catgtcattt agtgattata gtcacaacat atacaatgct gtatatgcca ttgctcatgc
1261 actccatgag aagaatctgc aagaagtTga aaatcaggca ataaacaatg cgaaaggaga
1321 aaatactcac tgcttgaagc taaactcatt tctgagaaag acccacttca ctaattctct
1381 tgggaacaga gtaattatga aacagagaga agtagtgcac ggagactata atattgttca
1441 catgttgaat ttctcacaac gccttgggat taaggTgaag ataggacaat tcagcccaca
1501 ttttccacag ggtcaacagt tacacttata tgtagacatg actgagttgg ctacaggaag
1561 tagaaagatg ccatcctcag tgtgcagtgc agattgccat cctggattca gaagaatctg
1621 gaaggaggaa atggcagcct gctgttttgt ttgcaacccc tgccctgaaa atgaaatttc
1681 taatgagacg atgggtggtat tttgggtctt cgtgaagcac catgacactc ctattgtgaa
1741 ggccaataac agaatcctca gctacctatt aatcgtgtca ctcatgttct gttttctgtg
1801 ctcccttttc ttcatTggct atcctaacag agcaacctgt atcttacagc aaatcacatt
1861 tggaaTcttc ttactgtgg ctatttccac agttctggcc aaaacaatca ctgtggttct
1921 ggctttcaaa gtcacagacc caggagaaca attaagaatc tttttggtat cggggacacc
1981 caactacatt attcccatg gttccctatt gcaatgtatt ctgtgtgcaa tctggctagc
2041 agttttctct cctttgttg atattgatga acactctgag catggccaca tcatcattgt
2101 gtgcaacaag ggctccatta ctgcattcta ctgtgtcctg ggatacttgg cctgcctggc
2161 ctttTgaagc ttcactatag ctttcttggc aaagaacctg cctgacacat tcaacgaagc
2221 caagttcttg accttcagca tgctagtgtt ctgcgctgtc tgggtcacct tcctccctgt
2281 ctaccatagc accaagggca aggtcatggt tgctgtggag atcttctcca tcttggcatc
2341 tagtgcaggg atgctgggat gcactttTgc acccaaagtt tacatcattt taatgagacc
2401 agacagaaat tcgatccaca aaatcaggga gaaatcatat ttctgaaaag gtatttcagg
2461 aattctgtca aatgtaaagt tgatacatac accccaaata tttagttaca gagcatatat
2521 ctagtTTtag aatcactctc actggttctc ctagttaagc atagaagtac catatgtact
2581 gatcttTcat atgttgtcta taaaatctta caatcattca tttgcttagt atcttctgga
2641 agaagtaaaa ttttcaaata actagtacaa ttttattcat tattttgctt tcatgaggat
2701 ttccccctgg taacttcaaa taaattttat aagtcagttg aatatataac cttacataga
2761 aagtgaTtTc taggacagac agggattata catagaaaca aactaactaa aaatcaacaa
2821 agatgaaatc agaacacatt ttcttatttc cagtaggaac acatacttga cagaatactg
2881 tctttttttc agctgctctt taagatatTg gccaatagtc taagtTaaa atgttcttta
2941 tctactctca aatacaaaaa tattatatcc aacaatggac agaactctgag aactcctgtg
3001 gttgagttag ggaatagttg gaagatactg agaaggaggt gacctatagg aatacaaaagc
3061 agtctcaact aacctggaca accaaggTcc ctgagacact gagccactaa caagtcagcc
3121 tactccagct gttatgaggc ccccaaaaaa tatgcaacat aggattgcct ggtccagcct
```

Figure 7  
Page 2 of 2

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3181 cagcaagaga atacacacct aaccacagag agacttcccc aagggttgg ggaggtctgg
3241 ggtttggaga gttgcggatt gtcccttgat gattggaagg aggtattgga tgagaatgaa
3301 tcagggggaa gactaggaag gggataatga tggaaactgta aaaaaaaaaa
```

SEQ ID NO:14  
Size: 380  
PRT FENI

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1 MGIQGLAKLI ADVAPSAIRE NDIKSYFGRK VAIDASMSIY QFLIAVRQGG DVLQNEEGET
61 TSHLMGMFYR TIRMMENGIK PVYVFDGKPP QLKSGELAKR SERRAEAEKQ LQQAQAAGAE
121 QEVEKFTKRL VKVTKQHNDK CKHLLSLMGI PYLDAPSEAE ASCAALVKAG KVVAAAATEDM
181 DCLTFGSPVL MRHLTASEAK KLPIQEFHLS RILQELGLNQ EQFVDLCILL GSDYCESIRG
241 IGPKRAVDLI QKHKSIEEIV RRLDPNKYPV PENWLHKEAH QLFLEPEVLD PESVELKWSE
301 PNEEELIKFM CGEKQFSEER IRSGVKRLSK SRQGSTQGRL DDFFKVTGSL SSAKRKEPEP
361 KGSTKKKAKT GAAGKFKRGK
```

Figure 8  
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SEQ ID NO:15  
Size: 4276  
DNA REV1

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1 agagccaccg cggagcgcgc gcggggttgg ttgccgcgag cgtgggggag cgtggaccgc
61 ggcgctgctc agcgggtgggg ctgccttccc cgggccctcc tccctggtec ctggcgaggg
121 cactggcggc ggcggggccg gggctccgaa ggccggagaa ggccggccgg cccgggcatg
181 gtggtctggg gcaacgcgga agaagctcca ccatgaggcg aggtggatgg aggaagcgag
241 ctgaaaatga tggctgggaa acatgggggt ggtatatggc tgccaagggt cagaaattgg
301 aggaacagtt tcgatcagat gctgctatgc agaaggatgg gacttcactc acaattttta
361 gtggagtggc catctatggt aatggatata cagatccttc cgctgaggaa ttgagaaaac
421 taatgatggt gcatggagggt caataccatg tatattattc cagatctaaa acaacacata
481 ttattgccac aaatcttccc aatgccaaaa ttaaagaatt aaagggggaa aaagtaattc
541 gaccagaatg gattgtggaa agcatcaaag ctggacgact cctctctac attccatata
601 agctgtacac caagcagtcc agtgtgcaga aaggctcag ctttaactct gtatgcagac
661 ctgaggatcc tctgccagggt ccaagcaata tagccaaaca gctcaacaac agggtaaatc
721 acatcggtta gaagattgaa acggaaaatg aagtcaaagt caatggcatg aacagttgga
781 atgaagaaga tgaaaataat gatttttagt ttgtggatct ggagcagacc tctccgggaa
841 ggaaacagaa tgggaattccg catcccagag ggagcactgc catttttaac ggacacactc
901 ctagctctaa tgggtgcctta aagacacagg attgcttggg gccctgggtc aacagtgttg
961 ccagcagggt ttctccagcc tttcccagg agggaggataa ggctgagaag agcagcactg
1021 atttcagaga ctgcactctg cagcagttgc agcaaagcac cagaaacaca gatgctttgc
1081 ggaatccaca cagaactaat tctttctcat tatcaccttt gcacagtaac actaaaatca
1141 atggtgctca ccactccact gttcaggggc cttcaagcac aaaagcact tcttcagtat
1201 ctacgtttag caaggcagca ccttcagtgc catccaaacc ttcagactgc aattttattt
1261 caaacttcta ttctcattca agactgcata acatatcaat gtggaagtgt gaattgactg
1321 agttttgtca taccctacaa agacaaagta atggtatctt tccaggaagg gaaaagttaa
1381 aaaaaatgaa aacaggcagg tctgcacttg ttgtaactga cacaggagat atgtcagtat
1441 tgaattctcc cagacatcag agctgtataa tgcagtgtga tatggattgc tctttgtat
1501 cagtgggtat acgaaataga ccagatctca aaggaaaacc agtggctgtt acaagtaaca
1561 gaggcacagg aagggcacct ttacgtcctg gcgctaaccc ccagctggag tggcagtatt
1621 accagaataa aatcctgaaa ggcaaagcag cagatatacc agattcatca ttgtgggaga
1681 atccagattc tgcgcaagca aatggaattg attctgtttt gtcaagggct gaaattgcat
1741 cttgtagtta tgaggccagg caacttggca ttaagaacgg aatgtttttt gggcatgcta
1801 aacaactatg tcctaactct caagctgttc catacgattt tcatgcatat aaggaagtgc
1861 cacaacatt gtatgaaaca ttggcaagct acactcataa cattgaagct gtcagtgtg
1921 atgaagcgct ggtagacatt accgaaatcc ttgcagagac caaacttact cctgtgaat
1981 ttgcaaatgc tgttcgtatg gaaatcaaag accagacgaa atgtgtgcc tctgttggaa
2041 ttggttctaa tattctcctg gctagaatgg caactagaaa agcaaaaacca gatgggcagt
2101 accacctaaa accagaagaa gtatagattt ttatcagagg ccagctagtg accaatctac
2161 caggagtggg acattcaatg gaatctaagt tggcatcttt gggaattaaa acttgtggag
2221 acttgcagta tatgaccatg gcaaaactcc aaaaagaatt tgggtcccaa acaggtcaga
2281 tgcttttatag gttctgccgt ggcttggatg atagaccagt tcgaactgaa aaggaaagaa
2341 aatctgtttc agctgagatc aactatggaa taaggtttac tcagccaaaa gaggcagaag
2401 cttttcttct gagtctttca gaagaaattc aaagaagact agaagccact ggcattgcaa
2461 gtaaacgtct aactctcaaa atcatggtac gaaagcctgg ggctcctgta gaaactgcaa
2521 aatttggagg ccatggaatt tgtgataaca ttgccaggac tgtaactctt gaccaggcaa
2581 cagataatgc aaaaataatt ggaaaggcga tgctaaacat gtttcataca atgaaactaa
2641 atatatcaga tatgagaggg gttgggattc acgtgaatca gttggttcca actaatctga
2701 acccttccac atgtcccagt cgcccatcag ttcagtcaag ccactttcct agtgggtcat
2761 actctgtccg tgatgtcttc caagttcaga aagctaagaa atccaccgaa gaggagcaca
2821 aagaagtatt tcgggctgct gtggatctgg aaatatcatc tgcttctaga acttgcactt
2881 tcttgcacc ttttcttgca catctgccga ccagtcctga tactaacaag gctgagtctt
2941 cagggaatg gaatggctca catactcctg tcagtgtgca gtcgagactt aacctgagta
3001 tagaggctcc gtcaccttcc cagctggatc agtctgtttt agaagcactt ccacctgatc
3061 tccgggaaca agtagagcaa gtctgtgctg tccagcaagc agagtccatc ggcgacaaaa
3121 agaaagaacc agtaaatggc tgtaatacag gaattttgcc acaaccagtt gggacagtct
3181 tgttgcaaat accagaacct caagaatcga acagtgcgc aggaataaat ttaatagccc
```

Figure 8  
Page 2 of 2

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3241 ttccagcatt ttcacaggtg gaccctgagg tatttgctgc ccttcctgct gaacttcaga
3301 gggagctgaa agcagcgat gatcaaagac aaaggcaggg cgagaacagc actcaccagc
3361 agtcagccag cgcactctgtg ccaaagaatc ctttacttca tctaaaggca gcagtgaaag
3421 aaaagaaaaa aaacaagaag aaaaaaacca ttggttcacc aaaaaggatt cagagtcctt
3481 tgaataacaa gctgcttaac agtcctgcaa aaactctgcc aggggcctgt ggcagtcctc
3541 agaagttaat tgatggggtt ctaaaacatg aaggacctec tgcagagaaa cccctggaag
3601 aactctctgc ttctacttca ggtgtgccag gcctttctag tttgcagtct gaccagctg
3661 gctgtgtgag acctccagca cccaatctag ctggagctgt tgaattcaat gatgtgaaga
3721 ccttgctcag agaatggata actacaattt cagatccaat ggaagaagac attctccaag
3781 ttgtgaaata ctgtactgat ctaataagaag aaaaagattt ggaaaaactg gatctagtta
3841 taaaatacat gaaaaggctg atgcagcaat cgggtggaatc gggttggaat atggcatttg
3901 actttattct tgacaatgtc cagggtggtt tacaacaaac ttatggaagc acattaaaag
3961 ttacataaat attaccagag agcctgatgc tctctgatag ctgtgccata agtgcttggtg
4021 aggtatttgc aaagtgcagt atagtaatgc tcggagtttt tataatttta aatttctttt
4081 aaagcaagtg ttttgtacat ttcttttcaa aaagtgcaa atttgtcagt attgcatgta
4141 aataattgtg ttaattattt tactgtagca tagattctat ttacaaaatg tttgtttata
4201 aagttttatg gattttttaca gtgaagtgtt tacagttgtt taataaagaa ctgtatgtaa
4261 aaaaaaaaaa aaaaaa
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SEQ ID NO:16  
Size: 1251  
PRT REV1

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1 MRRGGWRKRA ENDGWETWGG YMAAKVQKLE EQFRSDAAMQ KDGTSSSTIFS GVAIYVNGYT
61 DPSAEELRKL MMLHGGQYHV YYSRSKTTHI IATNLPNAKI KELKGEKVIR PEWIVESIKA
121 GRLLSYIPYQ LYTKQSSVQK GLSFNPVCRP EDPLPGPSNI AKQLNNRVNH IVKKIETENE
181 VKVNGMNSWN EEDENNDFSF VDLEQTSFGR KQNGIPHPRG STAIFNGHTP SSNGALKTQD
241 CLVPMVNSVA SRLSPAFSQE EDKAEKSTD FRDCTLQQLQ QSTRNTDALR NPHRTNSFSL
301 SPLHSNTKIN GAHHSTVQGP SSTKSTSSVS TFSKAAPSV SKPSDCNFIS NFYSHSRLHH
361 ISMWKCELTE FVNTLQRQSN GIFPGREKLK KMKTGRSALV VTDTGDMSVL NSPRHQSCIM
421 HVDMDCCFFVS VGIRNRPDLK GKPVAVTSNR GTGRAPLRPG ANPQLEWQYY QNKILKGKAA
481 DIPDSSLWEN PDSAQANGID SVLSRAEIAS CSYEARQLGI KNGMFFGHAK QLCPNLQAVP
541 YDFHAYKEVA QTLYETLAS THNIEAVSCD EALVDITEIL AETKLTPDEF ANAVRMEIKD
601 QTKCAASVGI GSNILLARMA TRKAKPDGQY HLPKEEVDDF IRGQLVTNLP GVGHSMESKL
661 ASLGIKTCGD LQYMTMAKLQ KEFGPKTGQM LYRFCRGLDD RPVRTEKERK SVSAEINYGI
721 RFTQPKAEAE FLLSLSEEIQ RRLEATGMKG KRLTLKIMVR KPGAPVETAK FGGHGICDNI
781 ARTVTLDQAT DNAKIIGKAM LNMFHTMKLN ISDMRGVGIH VNQLVPTNLN PSTCPSRPSV
841 QSSHFPSPGSY SVRDVFQVQK AKKSTEEHKK EVFRAAVDLE ISSASRTCTF LPPFPAHLPT
901 SPDTNKAESS GKWNGLHTPV SVQSRLNLSI EVSPSPQLDQ SVLEALPPDL REQVEQVCAV
961 QQAESHGDKK KEPVNGCNTG ILPQPVGTVL LQIPEPQESN SDAGINLIAL PAFSQVDPEV
1021 FAALPAELQR ELKAAVDQQR ROGENSTHQQ SASASVPKNP LLHLKAAVKE KKRNNKKKTI
1081 GSPKRIQSPL NNKLLNSPAK TLPGACGSPQ KLIDGFLKHE GPPAEKPLEE LSASTSGVPG
1141 LSSLQSDPAG CVRPPAPNLA GAVEFNDVKT LLREWITTIS DPMEEDILQV VKYCTDLIEE
1201 KDLEKLDLVI KYMKRLMQQS VESVWNMAFD FILDNVQVVL QQTYGSTLKV T
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Figure 9  
Page 1 of 2

SEQ ID NO:17  
Size: 2957  
DNA APEI

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1 ctgcagatag cactgggaaa gacaccgcgg aactcccgcg agcgagaccc gccaaaggccc
61 ctccagggac ctgtcttctt aacgtccagg gagcccagag caactcgcgc cttacattcg
121 tatccgtttt cctatctctt tcccgtggtc agcccagcct tctccactgt ttttttccctc
181 ttgcacagag ttagaatctt aagtcagtgt cacacaatgt gctgtgcac tggcacaacg
241 ataaacagcc gagggagggg tggggactaa gtgcctagag aattagagga gggaggcgag
301 gctaagcgtc cgtcacgtgg tgtcagacag accaatcacg cgcattcttc ggccacgaca
361 agcgcgcctc tgatcacgtg accagggtccg ctaccacagt ggggggtcag cgtgcacccct
421 tctttgtgct cgggttagga ggagctaggc tgccatcggg ccggtgcaga tacgggggtg
481 ctcttttgct cataagaggg gcttcgctgg cagtctgaac ggcaagcttg agtcaggacc
541 cttaattaag atcctcaatt ggctggaggg cagatctcgc gagtagggta caaggcacta
601 tgaatgatc tagtttcgtg ggtgaggggc tgaagggcct atgatgcacg gaggcgggga
661 aaggatttag agataacgtg gtttaaaggc gggacctggg gcggggagcg tccttggggag
721 gagtcttctc ccagccttag ctggtttcat gatttctttg cgtctgtagg caacgcggta
781 aaaatattgc ttcggtgggt gacgcggtag agctgcccag gggcggtcgt aacgggaatg
841 ccgaagcgty ggaaaaaggg agcggtgggc gaagacgggg atgagctcag gacaggtaag
901 ggaatgaaat cagcccttct tcttagaagc tgcggcgggg gtgtttgtca tcccttgat
961 gtacggtaag tacgggccga ctcatTTTTg caggggtttg tgaagaagtc gcaggaaccg
1021 taggctttcg ttgggtctat agttaacgcc ggatcgcagt tggaaaccac cagctttttg
1081 tcagtatata ttactcattt tatagagcca gaggccaaga agagtaagac ggccgcaaag
1141 aaaaatgaca aagaggcagc aggagagggc ccagccctgt atgaggaccc ccagatcag
1201 aaaacctcac ccagtggcaa acctgccaca ctcaagatct gctcttggaa tgtggatggg
1261 cttcgagcct ggattaagaa gaaaggatta gatgtgagtg gaatttgagg gaaagagaca
1321 ttttttagta ttgaatggtc ttagggttta gtcacccctt ttctcgttt agccttcagg
1381 ctgttttatt tttctcctgc ccgtagtttt ctgtggggct tcccagtcgt tgccagttgt
1441 atttcttaaa tgtctgttcc ttcaactcca ttgccatttt cttttttagt gttctctcct
1501 cttcccagaa tgttgcaaaa acctcttcac tatacttctt ccattttatc ttctgcatt
1561 gcattccata tgaagcatgt cctccattcc attaacata gcttaaaatc ttagcttgcct
1621 atccactgcc tatagaaaaa acacatctcc ttggcatagc atgtaagact ttcttacctc
1681 tctatatttg ttttcattta tctagcttag aattgtttga atattgtgct gcttgactcg
1741 aactccttag gccaaagagc tgtttaacct gtgcgtatct atgacttagc atatagatta
1801 ttcaataaat gttctgctga attgataata cgttttccac ctttcttttc acttacagtg
1861 ggtaaaaggaa gaagcccagc atatactgtg cttcaagag accaaatggt cagagaacaa
1921 actaccagct gaacttcagg agctgcctgg actctctcat caatactggg cagctccttc
1981 ggacaaggaa gggtagagtg gcgtgggcct gctttccgcg cagtgcacac tcaaagtttc
2041 ttacggcata ggtgagaccc tattgatgcc taatgcctga actcttcaaa accaattgct
2101 aattctctat ctctgcccc aactcttgatt gctttccctt ttcttatagt tttttatgct
2161 aattctgttt catttctata ggcgatgagg agcatgatca ggaaggccgg gtgattgtgg
2221 ctgaatttga ctggtttgtg ctggtaacag catatgtacc taatgcaggc cgaggctcgg
2281 tacgactgga gtaccggcag cgtgggatg aagcctttcg caagtctctg aagggcctgg
2341 cttcccgaag gcccttgtg ctgtgtggag acctcaatgt ggcacatgaa gaaattgacc
2401 ttcgcaaccc caaggggaac aaaaagaatg ctggcttcac gccacaagag cgccaaggct
2461 tcggggaatt actgcaggct gtgccactgg ctgacagctt taggcaacct taccccaaca
2521 caccctatgc ctacaccttt tggacttata tgatgaatgc tcgatccaag aatgttggtt
2581 ggcgccttga ttactttttg ttgtccact ctctgttacc tgcattgtgt gacagcaaga
2641 tccgttccaa ggccctcggc agtgatcact gtccatcac cctataccta gcaactgtgac
2701 accacccta aatcactttg agcctgggaa ataagcccc tcaactacca ttcttcttt
2761 aaacactctt cagagaaatc tgcattctat ttctcatgta taaaactagg aatcctccaa
2821 ccaggctcct gtgatagagt tcttttaagc ccaagatttt ttatttgagg gttttttgtt
2881 ttttaaaaaa aaattgaaca aagactacta atgactttgt ttgaattatc cacatgaaaa
2941 taaagagcca tagtttc
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Figure 9  
Page 2 of 2

SEQ ID NO:18  
Size: 318  
PRT APE1

1	MPKRGKKGAV	AEDGDEL RTE	PEAKKSKTAA	KKNDKEAAGE	GPALYEDPPD	QKTSPSGKPA
61	TLKICSWNVD	GLRAWIKKKG	LDWVKEEAPD	ILCLQETKCS	ENKLPAELQE	LPGLSHQYWS
121	APSDKEGYSG	VGLLSRQCPL	KVSYGIGDEE	HDQEGRVIVA	EFDSFVLVTA	YVPNAGRGLV
181	RLEYRQRWDE	AFRKFLKGLA	SRKPLVLCGD	LNVAHEEIDL	RNPKGNKKNA	GFTPQEAQGF
241	GELLQAVPLA	DSFRHLYPNT	PYAYTFWTYM	MNARSKNVGW	RLDYFLLSHS	LLPALCDSKI
301	RSKALGSDHC	PITLYLAL				



Figure 10

SEQ ID NO:19  
Size: 1161  
DNA CDK3

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1 ccacatggaa gctggaggag caaccgggag cgctgggctg gggtgcaaat tgcccagtgc
61 cttctgtttc ccaggcagct ctgtggccat ggatatgttc cagaaggtag agaagatcgg
121 agagggcacc tatggggtgg tgtacaaggc caagaacagg gagacagggc agctggtggc
181 cctgaagaag atcagactgg atttggagat ggaggggggtc ccaagcactg ccatcaggga
241 gatctcgctg ctcaaggaac tgaagcacc caacatcgtc cgactgctgg acgtggtgca
301 caacgagagg aagctctatc tgggtgtttga gttcctcagc caggacctga agaagtacat
361 ggactccacc ccaggctcag agctccccct gcacctcatc aagagctacc tcttccagct
421 gctgcagggg gtgagtttct gccactcaca tcgggtcatc caccgagacc tgaagcccca
481 gaacctgctc atcaatgagt tgggtgccat caagctggct gacttcggcc tggctcgcg
541 cttcgggggtg cccctgcgca cctacacca tgaggtgggtg acactgtggt atcgcgcccc
601 cgagattctc ttgggcagca agttctatac cacagctgtg gatattctga gcattggttg
661 catcttttga gagatggtga ctcgaaaagc cctgtttcct ggtgactctg agattgacca
721 gctcttttct atctttcgta tgctggggag acccagcgaa gacacatggc ccggggtcac
781 ccagctgcct gactataagg gcagcttccc taagtggacc aggaagggac tgaagagat
841 tgtgccaat ctggagccag agggcagggg cctgctcatg caactcctgc agtatgacc
901 cagccagcgg atcacagcca agactgcctt ggcccacccg taacttctcat cccctgagcc
961 ctccccagct gcccgccagt atgtgctgca gcgattccgc cattgagaat gtcaaggcca
1021 cactcagatc ctttctcgag cagcagctgc tgccccagct gcctcctacc cattgccaag
1081 agaggatgca tctggggaga gcaaagcact aaggaattca gcatcagcct gcagagggct
1141 gagtctgggt tagtcctgcc c

```

SEQ ID NO:20  
Size: 305  
PRT CDK3

```

1 MDMFQKVEKI GEGTYGVVYK AKNRETGQLV ALKKIRLDLE MEGVPSTAIR EISLLKELKH
61 PNIVRLLDVV HNERKLYLVF EFLSQDLKKY MDSTPGSELP LHLIKSYLFQ LLQGVSFCHS
121 HRVIHRDLKP QNLLINELGA IKLADFGLAR AFGVPLRITY HEVVTWLYRA PEILLGSKFY
181 TTAVDIWSIG CIFAEMVTRK ALFPGDSEID QLFRIFRMLG TPSEDTPWPGV TQLPDYKGSF
241 PKWTRKGLLE IVPNLEPEGR DLLMQLLQYD PSQRITAKTA LAHPYFSSPE PSPAARQYVL
301 QRFRH

```

Figure 11

SEQ ID NO:21

Size: 2297

DNA PIMI

```

1  gcgccgcac  ctggagggtg  ggatgctctt  gtccaaaatc  aactcgcttg  cccacctgcg
61  cgcgcgcgcc  tgcaacgacc  tgcacgccac  caagctggcg  cggggcaagg  agaaggagcc
121  cctggagtcg  cagtaccagg  tgggcccgcg  actgggcagc  ggcggcttcg  gctcgggtcta
181  ctcaggcatc  cgcgtctccg  acaacttgcc  ggtggccatc  aaacacgtgg  agaaggaccg
241  gatttccgac  tggggagagc  tgcctaattg  cactcgagtg  cccatggaag  tggctctgct
301  gaagaagggtg  agctcgggtt  tctccggcgt  cattaggctc  ctggactggg  tcgagaggcc
361  cgacagtttc  gtctgatcc  tggagaggcc  cgagccgggtg  caagatctct  tcgacttcat
421  cacggaaagg  ggagccctgc  aagaggagct  ggcccgcagc  ttcttctggc  aggtgctgga
481  ggccgtgcgg  cactgccaca  actgcggggt  gctccaccgc  gacatcaagg  acgaaaacat
541  ccttatcgac  ctcaatcgcg  gcgagctcaa  gctcatcgac  ttcgggtcgg  gggcgtgct
601  caaggacacc  gtctacacgg  acttcgatgg  gacccgagtg  tatagccctc  cagagtggat
661  ccgctaccat  cgctaccatg  gcaggtcggc  ggcagttctg  tccctgggga  tcctgctgta
721  tgatattggtg  tgtggagata  ttcttttcga  gcatgacgaa  gagatcatca  gggggccagg
781  tttcttcagg  cagagggtct  cttcagaatg  tcagcatctc  attagatggg  gcttggccct
841  gagaccatca  gataggccaa  ccttcgaaga  aatccagaac  catccatgga  tgcaagatgt
901  tctcctgccc  caggaaactg  ctgagatcca  cctccacagc  ctgtcgccgg  ggcccagcaa
961  atagcagcct  ttctggcagg  tctcccccct  tcttgtcaga  tgcccaggag  ggaagcttct
1021  gtctccagct  ttcccagata  ccagtgcac  gtctcgccaa  gcaggacagt  gcttgataca
1081  ggaacaacat  ttacaactca  ttccagatcc  caggcccctg  gaggctgcct  cccaacagtg
1141  ggaagagtg  actctccagg  ggtcctaggc  ctcaactcct  cccatagata  ctctcttctt
1201  ctcatagggtg  tccagcattg  ctggactctg  aaatatcccg  ggggtggggg  gtgggggtgg
1261  gtcagaaccc  tgccatggaa  ctgtttcctt  catcatgagt  tctgctgaat  gccgcgatgg
1321  gtcaggtagg  ggggaaacag  gttgggatgg  gataggacta  gcaccatttt  aagtccctgt
1381  caccctctcc  gactctttct  gagtgccttc  tgtggggact  ccggctgtgc  tgggagaaat
1441  acttgaactt  gcctctttta  cctgctgctt  ctccaaaaat  ctgcctgggt  tttgttccct
1501  atttttctct  cctgtctctc  ctaccccctt  ccttcatatg  aaaggtgcca  tggaagaggc
1561  tacagggcca  aacgctgagc  cactgcctct  tttttctcct  ccttttagtaa  aactccgagt
1621  gaactgggtct  tccttttttg  tttttactta  actgtttcaa  agccaagacc  tcacacacac
1681  aaaaaatgca  caaacaatgc  aatcaacaga  aaagctgtaa  atgtgtgtac  agttggcatg
1741  gtagtatata  aaaagattgt  agtggatcta  atttttaaga  aattttgcct  ttaagttatt
1801  ttacctgttt  ttgtttcttg  ttttgaaaga  tgcgcattct  aacctggagg  tcaatgttat
1861  gtattttatt  atttatttat  ttggttccct  tctannnnnn  nnnnnngctg  ctgccttagt
1921  tttctttcct  cctttctctc  tctgacttgg  ggaccttttg  ggggagggtg  gcgacgcttg
1981  ctctgtttgt  ggggtgacgg  gactcaggcg  ggacagtgtc  gcagctccct  ggcttctgtg
2041  gggcccctca  cctacttacc  cagggtgggtc  ccggtctgtg  ggggtgatggg  gaggggcatt
2101  gctgactgtg  tatataggat  aattatgaaa  agcagttctg  gatgggtgtgc  cttccagatc
2161  ctctctgggg  ctgtgttttg  agcagcagg  agcctgctgg  ttttatctga  gtgaaatact
2221  gtacagggga  ataaaagaga  tcttattttt  ttttttatac  ttggcgtttt  ttgaataaaa
2281  accttttgtc  ttaaaac

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SEQ ID NO:22

Size: 313

PRT PIMI

```

1  MLLSKINSLA  HLRARACNDL  HATKLAPGKE  KEPLESQYQV  GPLLGSGGFG  SVYSGIRVSD
61  NLPVAIKHVE  KDRISDWGEL  PNGTRVPM EV  VLLKKVSSGF  SGVIRLLDWF  ERPDSFVLIL
121  ERPEPVQDLF  DFITERGALQ  EELARSFFWQ  VLEAVRHCHN  CGVLHRDIKD  ENILIDLNRG
181  ELKLIDFGSG  ALLKDTVYTD  FDGTRVYSPP  EWIRYHRYHG  RSAAVWSLGI  LLYDMVCGDI
241  PFEHDEEII  R  QGVFFRQ RVS  SECQHLIRWC  LALRPSDRPT  FEEIQNH PPM  W  QDVLLPQETA
301  EIHLSLSPG  PSK

```

Figure 12  
Page 1 of 2

SEQ ID NO:23  
Size: 3178  
DNA CDC7L1

```
1 gatctcttgg agacggcgac ccaggcatct ggggagccac agaagtcgta ctcccttaaa
61 ccctgctttg ctccccctgt ggatgtaacc ccttagctgg cattttgcat ctcaattggc
121 ttgtgatgga ggcgtctttg gggattcaga tggatgagcc aatggctttt tctccccagc
181 gtgaccggtt tcaggctgaa ggctctttta aaaaaaacga gcagaatttt aaacttgcag
241 gtgttaaaaa agatattgag aagctttatg aagctgtacc acagcttagt aatgtgttta
301 agattgagga caaaattgga gaaggcactt tcagctctgt ttatttggcc acagcacagt
361 tacaagtagg acctgaagag aaaattgctc taaaacactt gattccaaca agtcatccta
421 taagaattgc agctgaactt cagtgcctaa cagtggctgg ggggcaagat aatgtcatgg
481 gagttaaata ctgctttagg aagaatgac atgtagttat tgctatgcca tatctggagc
541 atgagtcggt tttggacatt ctgaattctc tttcctttca agaagtacgg gaatatatgc
601 ttaatctgtt caaagctttg aaacgcattc atcagtttgg tattgttcac cgtgatgtta
661 agcccagcaa ttttttatat aataggcgcc tgaaaaagta tgccttggtg gactttgggt
721 tggcccaagg aacctatgat acgaaaatag agcttcttaa atttgtccag tctgaagctc
781 agcaggaaag gtgttcacaa aacaaatccc acataatcac aggaacaag attccactga
841 gtggcccgat acctaaggag ctggatcagc agtccaccac aaaagcttct gttaaaagac
901 cctacacaaa tgcacaaatt cagattaaac aaggaaaaga cggaaaggag ggatctgtag
961 gcctttctgt ccagcgctct gtttttggag aaagaaattt caatatcac agctccattt
1021 cacatgagag cctgcagtg aaactcatga agcagtcaaa gactgtggat gtactgtcta
1081 gaaagttagc aacaaaaaag aaggctatct ctacgaaagt tatgaatagt gctgtgatga
1141 ggaaaactgc cagttcttgc ccagctagcc tgacctgtga ctgctatgca acagataaag
1201 tttgtagtat ttgcctttca aggcgtcagc aggttgcccc tagggcagg acaccaggat
1261 tcagagcacc agaggtcttg acaaagtgcc ccaatcaaac tacagcaatt gacatgtggt
1321 ctgcagggtg catatttctt tctttgctta gtggacgata tccattttat aaagcaagtg
1381 atgatttaac tgctttggcc caaattatga caattagggg atccagagaa actatccaag
1441 ctgctaaaac ttttgggaaa tcaatattat gtagcaaaga agttccagca caagacttga
1501 gaaaactctg tgagagactc aggggtatgg attctagcac tccaagtta acaagtgata
1561 tacaagggca tgcttctcat caaccagcta tttcagagaa gactgaccat aaagcttctt
1621 gcctcgttca aacacctcca ggacaatact cagggaattc atttaaaaag ggggatagta
1681 atagctgtga gcattgtttt gatgagtata ataccaattt agaaggctgg aatgaggtag
1741 ctgatgaagc ttatgacctg cttgataaac ttctagatct aaatccagct tcaagaataa
1801 cagcagaaga agctttgttg catccatttt ttaaagatat gagcttgtga taatggatct
1861 tcatttaatg tttactgtta tgaggtagaa taaaaagaa tactttgtaa tagccacaag
1921 ttcttgttta gagaccagag caggattaat aatttatttt aacattttag tgtttggtgg
1981 cacattctaa aatatagatt aagaatactt aaaatgcctg ggatagttct tgggactaac
2041 aacatgatct tctttgagtt aaacctacct aagtagattt taggtgggtt ccttatagg
2101 cagattttta gcttccttaa ttacctttca ctgacataca gaaaaaggag cagttttagt
2161 ttttaattaat taaaattaac agatgtgatg aggattaaat gaatcaaaag acttaatttg
2221 tagattcttt tagagttatg agctaggtat agtttgggga aactcaacct ggtgctggtg
2281 ctcttaacaa ttttgtaaat aaagaagata atttcctttt ctagaggtag atattaggcc
2341 ttttatgaac actaaaacaa tgaggaaatg ttggtcatgg ggcaaagtat cacttaaaat
2401 tgaattcatc cattttttaa aaacacttca tgaaagcatt ctggtgtgaa ttgccatttt
2461 tttcttactg gcttctcaat tttcttctt ctctgcccc acctaaaaca ttctctcctg
2521 aaattacatg gtgctgacca caaagtttct ggatgtttta ttaaatttg tacgtgttta
2581 cagttgggaa tttaaaataa tacatacact ggttgataaa gggaaagctg aggaccaagg
2641 tgaagattga tagtccaaat gcttttcttt tttgagttgt atattttttc acaccatctt
2701 agatataatt aggtagctgc tgaaaggaaa agtgaataca gaattgacgg tattatttga
2761 gatttttctt ctgcgtagag ccattccagat ctctgtatcc tgttttgact aagtcttagg
2821 tgggttggga agacagataa tgaagtaggc aaagagaaaa ggaccaaga tagaggttta
2881 tattcagaaa tggatatata caatgacagc atatcaaact tcctatggga aaaagtctgg
2941 tgggtgggca gctgacagat ttcccattta gtagtcatag aatacagaaa tagtttaggg
3001 acatgtattc attttgttat tttgagctta gataggctag tatatctacc taatctgttt
3061 ggtaagtata ggatatataa accattacca ttgatctgtc ttatgccata atcttaaaaa
3121 aaaattgaat gctcttgaat ttgtatatcc aataaagtta tccttttata aaaaaaaa
```

Figure 12  
Page 2 of 2

SEQ ID NO:24  
Size: 574  
PRT CDC7L1

```
1 MEASLGIQMD EPMAFSPQRD RFQAEGLKK NEQNFKLAGV KKDIEKLYEA VPQLSNVFKI
61 EDKIGEGTFS SVYLATAQLQ VGPEEKIALK HLIPTSHPIR IAAELQCLTV AGGQDNVMGV
121 KYCFRKNDHV VIAMPYLEHE SFLDILNSLS FQEVREYMLN LFKALKRIHQ FGIVHRDVKP
181 SNFLYNRRLLK KYALVDFGLA QGTHDTKIEL LKFVQSEAQQ ERCSQNKSHI ITGNKIPLSG
241 PVPKELDQQS TTKASVKRPY TNAQIQIKQG KDGKEGSVGL SVQRSVFGER NFNHSSISH
301 ESPAVKLMKQ SKTVDVLSRK LATKKKAIST KVMNSAVMRK TASSCPASLT CDCYATDKVC
361 SICLSRRQQV APRAGTPGFR APEVLTKCPN QTTAIDMWSA GVIFLSLLSG RYPFYKASDD
421 LTALAQIMTI RGSRETIQAA KTFGKSILCS KEVPAQDLRK LCERLRGMDS STPKLTSDIQ
481 GHASHQPAIS EKTDHKASCL VQTPPGQYSG NSFKKGDSNS CEHCFDEYNT NLEGWNEVPD
541 EAYDLLDKLL DLNPASRITA EEALLHPFFK DMSL
```

Figure 13

SEQ ID NO:25  
Size: 1427  
DNA CDK7

```

1  tgggtgttgg aggcctttaag gtagctttaa attcgtgttg tcctgggagc tcgccctttt
61  cggctggagt cgggcctttac ggcgccggat ggctctggac gtgaagtctc gggcaaagcg
121 ttatgagaag ctggacttcc ttggggaggg acagtttgcc accgtttaca aggccagaga
181 taagaatacc aaccaaattg tcgccattaa gaaaatcaaa cttggacata gatcagaagc
241 taaagatggg ataaatagaa ccgccttaag agagataaaa ttattacagg agctaagtca
301 tccaaatata attggtctcc ttgatgcttt tggacataaa tctaattatta gccttgtctt
361 tgattttatg gaaactgata tagaggttat aataaaggat aatagtcttg tgctgacacc
421 atcacacatc aaagcctaca tgttgatgac tcttcaagga ttagaatatt tacatcaaca
481 ttggatccta catagggatc tgaaaccaa caacttggtg ctagatgaaa atggagtctt
541 aaaactggca gattttggcc tggccaaatc ttttgggagc cccaatagag cttatacaca
601 tcaggttgta accagggtgg atcgggcccc cgagttacta tttggagcta ggatgtatgg
661 tgtagggtgt gacatgtggg ctggttgctg tatattagca gagttacttc taagggttcc
721 ttttttgcca ggagattcag acctgatca gctaacaaga atatttgaaa ctttgggcac
781 accaactgag gaacagtggc cggacatgtg tagtcttcca gattatgtga catttaagag
841 tttccctgga atacctttgc atcacatctt cagtgcagca ggagacgact tactagatct
901 catacaaggc ttattcttat ttaatccatg tgctcgaatt acgcccacac aggcactgaa
961 aatgaagtat ttcagtaatc ggccagggcc aacacctgga tgtcagctgc caagacaaaa
1021 ctgtccagtg gaaaccttaa aggagcaatc aaatccagct ttggcaataa aaaggaaaag
1081 aacagaggcc ttagaacaag gaggattgcc caagaaacta attttttaaa gagaacactg
1141 gacaacattt tactactgag ggaaatagcc aaaaaggcaa ataatggaaa aatagtaaac
1201 attaagtaaa tgctgtagaa gtgagtttgt aaatattcta cacatgtaaa atatgtaaaa
1261 ctatgggtta tttttattaa atgtatttta aaataaaaaa ttaattctgg tttttctgat
1321 tagagtccca aagtgagaaa agttcaatac tcttgaaatg tagaattgaa aatgcattag
1381 ggaaaactta ataaaaatta ttaccagtta tttggaaaaa aaaaaaa

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SEQ ID NO:26  
Size: 346  
PRT CDK7

```

1  MALDVKSRAK RYEKLDLFLGE GQFATVYKAR DKNTNQIVAI KKIKLHRSE AKDGINRTAL
61  REIKLLQELS HPNIIGLLDA FGHKSNISLV FDFMETDLEV IIKDNSLVLT PSHIKAYMLM
121 TLQGLEYLHQ HWILHRDLKP NNLLLDENG V LKLADFLAK SFGSPNRAYT HQVVTRWYRA
181 PELLFGARMY GVGVDMWAVG CILAEALLRV PFLPGDSDL QLTRIFETLG TPTEEQWPD
241 CSLPDYVTFK SFPGIPLHHI FSAAGDLDL LIQGLFLFNP CARITATQAL KMKYFSNRPG
301 PTPGCQLPRP NCPVETLKEQ SNPALAIKRK RTEALEQGGL PKKLIF

```

Figure 14

SEQ ID NO:27  
Size: 2169  
DNA CNK

```

1  ccgcctccga gtgccttgcg cggacctgag ctggagatgc tggccgggct accgacgtca
61  gaccccgggc gcctcatcac ggacccgcgc agcggccgca cctacctcaa aggccgcttg
121 ttgggcaagg ggggcttcgc ccgctgctac gaggccactg acacagagac tggcagcgcc
181 tacgctgtca aagtcatccc gcagagccgc gtcgccaagc cgcatacagc cgagaagatc
241 ctaaattgaga ttgagctgca ccgagacctg cagcaccgcc acatcgtgcg tttttcgcac
301 cacttttgagg acgctgacaa catctacatt ttcttgagac tctgcagccg aaagtccctg
361 gccacatctt ggaaggcccc gcacaccctg ttggagccag aagtgcgcta ctacctgcgg
421 cagatccttt ctggcctcaa gtacttgcac cagcgcggca tcttgaccg ggacctcaag
481 ttgggaaatt ttttcatcac tgagaacatg gaactgaagg tgggggattt tgggctggca
541 gcccggttgg agcctccgga gcagaggaag aagaccatct gtggcaccct caactatgtg
601 gctccagaag tgctgctgag acagggccac ggccctgaag cggatgtatg gtcactgggc
661 tgtgtcatgt acacgctgct ctgcgggagc cctccctttg agacggctga cctgaaggag
721 acgtaccgct gcatcaagca ggttcactac acgctgcctg ccagcctctc actgcctgcc
781 cggcagctcc tggccgccat ccttcggggc taccgccgag accgcccctc tattgaccag
841 atcctgcgcc atgacttctt taccaagggc tacaccccg atcgactccc tatcagcagc
901 tgcgtgacag tcccagacct gacacccccc aaccagcta ggagtctgtt tgccaaagtt
961 accaagagcc tctttggcag aaagaagaag agtaagaatc atgccagga gagggatgag
1021 gtctccggtt tgggtgagcg cctcatgcgc acatocgttg gccatcagga tgccaggcca
1081 gaggctccag cagcttcttg cccagccctt gtcagcctgg tagagacagc acctgaagac
1141 agctcaccct gtgggacact ggcaagcagt ggagatggat ttgaagaagg tctgactgtg
1201 gccacagtag tggagtgcgc cctttgtgct ctgagaaatt gtatagcttt catgccccca
1261 gcggaacaga acccgcccc cctggcccag ccagagcctc tgggtgpggt cagcaagtgg
1321 gttgactact ccaataagtt cggttttggg tatcaactgt ccagccgccc tgtggtgtg
1381 ctcttcaacg atggcacaca tatggccctg tcggccaaca gaaagactgt gactacaat
1441 cccaccagca caaagcactt ctcttctctc gtgggtgctg tgccccgggc cctgcagcct
1501 cagctgggta tctgcggta cttgcctccc tacatggagc agcacctcat gaaggggtgga
1561 gatctgcccc gtgtggaaga ggtagaggta cctgctccgc ccttgcctgt gcagtgggtc
1621 aagacggatc aggtctctct catgctgttt agtgatggca ctgtccaggt gaacttctac
1681 ggggaccaca ccaagctgat tctcagtggc tgggagcccc tccttgtgac ttttgtggcc
1741 cgaaatcgta gtgcttgtag ttacctcgct tcccacctc ggcagctggg ctgctctcca
1801 gacctgcggc agcgactccg ctatgctctg cgctgctccc gggaccgcag cccagcttag
1861 gacccaagcc ctgaaggcct gaggcctgtg cctgtcaggc tctggccctt gcctttgtgg
1921 ccttccccct tcctttggtg cctcactggg ggctttgggc cgaatcccc agggaatcag
1981 ggaccagctt tactggagtt gggggcggct tgtcttcgct ggctcctacc ccatctccaa
2041 gataagcctg agccttagct cccagctagg gggcggtatt tatggaccac ttttatttat
2101 tgtcagacac ttattttatt ggatgtgagc cccagggggc ctctcctag gataataaac
2161 aattttgca

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SEQ ID NO:28  
Size: 607  
PRT CNK

```

1  MLAGLPTSDP GRLITDPRSG RTYLKGRLLG KGGFARCYEA TDTETGSAYA VKVIPQSRVA
61  KPHQREKILN EIELHRDLQH RHIVRFSSHFF EDADNIYIFL ELCSRKSLAH IWKARHTLLE
121 PEVRYYLROI LSGLKYLHQR GILHRDLKLG NFFITENMEL KVGDFGLAAR LEPPEQRKKT
181 ICGTPNYVAP EVLLRQGHGP EADVWSLGCV MYTLLCGSPP FETADLKETY RCIKQVHYTL
241 PASLSLPAEQ LLAAILRASP RDRPSIDQIL RHDFFTKGYT PDRLPISSCV TVPDLTPPNP
301 ARSLFAKVTK SLFGRKKKSK NHAQERDEVS GLVSGLMRTS VGHQDARPEA PAASGPAPVS
361 LVETAPEDSS PRGTLASSGD GFEEGLTVAT VVESALCALR NCIAFMPPAE QNPAPLAQPE
421 PLVWVSKWVD YSNKFGFGYQ LSSRRVAVLF NDGTHMALSA NRKTVHYNPT STKHFSFSVG
481 AVPRALQPQL GILRYFASYM EQHLMKGGDL PSVEEVEVPA PPLLLQWVKT DQALLMLFSD
541 GTVQVNFYGD HTKLILSGWE PLLVTFVARN RSACTYLASH LRQLGCSPDL RQRLRYALRL
601 LRDRSPA

```

Figure 15

SEQ ID NO:29

Size: 1321

DNA PRL-3

```

1  tgactatcca gctctgagag acgggagttt ggagttgccc gctttacttt ggttgggttg
61  gggggggcgg cgggctgttt tggttcctttt cttttttaag agttgggttt tcttttttaa
121 ttatccaaac agtgggcagc ttctccccc acaccaagt atttcacaa tatttgtagc
181 gggatatggg gtgggttttt aaatctcggt tctcttgga aagcacagg atctcggtct
241 cctcattttt tgggggtgtg tggggacttc tcaggtcgtg tcccagcct tctctgcagt
301 cccttctgcc ctgccgggcc cgtcgggagg cgccatggct cggatgaacc gcccggcccc
361 ggtggagggt agctacaaac acatgcgctt cctcatcacc cacaaccca ccaacgccac
421 gctcagcacc ttcattgagg acctgaagaa gtacggggct accactgtgg tgcgtgtgtg
481 tgaagtgacc tatgacaaaa cgccgctgga gaaggatggc atcaccttg tggactggcc
541 gtttgacgat ggggcgcccc cgcccgcaa ggtagtggaa gactggctga gcctggtgaa
601 ggccaagttc tgtgaggccc ccggcagctg cgtggctgtg cactgcgtgg cgggcctggg
661 ccggaagcgc cgcggagcca tcaacagcaa gcagctcacc tacctggaga aataccggcc
721 caaacagagg ctgcggttca aagaccaca cacgcacaag acccgtgct gcgttatgta
781 gctcaggacc ttggtgggct ctggtcgtca tgtaggtcag gacctggct ggacctggag
841 gccctgcccc gccctgctct gccagccca gcaggggctc caggccttg ctggccccac
901 atcgctttt cctccccgac acctccgtgc acttgtgtcc gaggagcgag gagcccctcg
961 ggccctgggt ggccctctgg ccctttctcc tgtctccgc actccctctg gcggcgctgg
1021 ccgtggctct gtctctctga ggtgggtcgg gcgccctctg ccgccccct cccacaccag
1081 ccaggtggt ctcctctagc ctgtttgttg tggggtgggg gtatatattg taaccactgg
1141 gccccagcc cctcttttgc gacccttgt cctgacctgt tctcggcacc ttaaattatt
1201 agaccccggt gcagtcaggt gctccggaca ccgaaggca ataaaacagg agccgtgaaa
1261 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
1321 a

```

SEQ ID NO:30

Size: 148

PRT PRL-3

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1  MARMNRPAPV EVSYKHMRF ITHNPTNATL STFIEDLK KY GATTVVVRCE VTYDKTPLEK
61  DGITVVDWPF DDGAPPGKV VEDWLSLVKA KFCEAPGSCV AVHCVAGLGR KRRGAINSKQ
121 LTYLEKYRPK QLRFKDPHT HKTRCCVM

```

Figure 16  
Page 1 of 2

SEQ ID NO:31  
Size: 3696  
DNA STK2 (NEK4)

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1 ggatcgctat ggcagcggcg tcgtcgcggg ccggggccca gcaatcccgc ccggggcccg
61 ctgcctcaac agccgcccc actgccccct ctcgggcatg aaccgagctt cttgttgccg
121 cccgctgccc taccgcccgc tgccgcccga tcccgaactc gggccagcgc tgggaacatg
181 cccctggccg cctactgcta cctgcgggtc gtgggcaagg ggagctatgg agaggtgacg
241 cttgtgaagc accggcggga cggcaagcag tatgtcatca aaaaactgaa cctccgaaat
301 gcctctagcc gagagcggcg agctgctgaa caggaagccc agctcttgct tcagttgaag
361 catcccaaca ttgtcaccta caaggagtca tgggaaggag gagatgggtc gctctacatt
421 gtcatgggct tctgtgaagg aggtgatttg taccgaaagc tcaaggagca gaaagggcag
481 cttctgcctg agaatcaggt ggtagagtgg tttgtacaga tcgcatggc tttgcagtat
541 ttacatgaaa aacacatcct tcatcgagat ctgaaaactc aaaaatgtct cctaacaaga
601 acaaactca tcaaagtagg ggacctagga attgcccag tgttagagaa ccactgtgac
661 atggctagca ccctcattgg cacaccctac tacatgagcc ctgaattgtt ctcaaacaaa
721 ccctacaact ataagtctga tgtttgggct ctaggatgct gtgtctatga aatggccacc
781 ttgaagcatg ctttcaatgc aaaagatatg aattctttag tttatcggat tattgaagga
841 aagctgccac caatgccaaag agattacagc ccagagctgg cagaactgat aagaacaatg
901 ctgagcaaaa ggctgaaga aaggccgtct gtgaggagca tcctgaggca gccttatata
961 aagcggcaaa tctccttctt tttggaggcc acaaagataa aaacctcaa aaataacatt
1021 aaaaatgggtg actctcaatc caagcctttt gctacagtgg tttctggaga ggcagaatca
1081 aatcatgaag taatccaccc ccaaccactc tcttctgagg gctcccagac atatataatg
1141 ggtgaaggca aatgtttgtc ccaggagaaa ccaggggcct ctggtctctt gaagtcacct
1201 gccagtctga aagcccatac ctgcaaacag gacttgagca ataccacaga actagccaca
1261 atcagtagcg taaatattga catcttacct gcaaaaggga gggattcagt gagtgatggc
1321 tttgttcagg agaatcagcc aagatatttg gatgcctcta atgagttagg aggtatatgc
1381 agtatttctc aagtggaaga ggagatgctg caggacaaca ctaaaccag tgcccagcct
1441 gaaaacctga ttcccatgtg gtccctctgac attgtcactg gggaaaagaa tgaaccagtg
1501 aagcctctgc agcccctaata caaagaacaa aagccaaagg accagagtct tgccctgtcg
1561 cccaagctgg agtgcagtgg cacaatcttg gctcacagca acctccgctt cgtgggttca
1621 agtgattctc cagcctcagc ctcccagagta gctgggatta caggcgtgtg ccaccagccc
1681 caggatcaag ttgctggtga atgtattata gaaaaacagg gcagaatcca ccagatttta
1741 cagccacaca actctgggtc tgaaccttcc ctgtctcgac agcgacggca aaagaggaga
1801 gaacagactg agcacagagg ggaaaagaga caggctccgca gagatctctt tgctttccaa
1861 gagtcgctc ctcgattttt gcctttctcat cccattgttg ggaaagtgga tgtcacatca
1921 acacaaaaag aggtgaaaa ccaacgtaga gtggtcactg ggtctgtgag cagttcaagg
1981 agcagtgaag tgtcatcacc aaaggatcga ccattatcag ccagagagag gaggcgacta
2041 aagcagtcac aggaagaaat gtctcttcca gccccttcag tgaggaaaag gtctctgagt
2101 gtagcagggc caggaaaacc ccaggaagaa gaccagccct tgctgcccg acggtctcc
2161 tctgactgca gcgtcactca ggaaaggaaa cagattcatt gtctgtctga ggatgagtta
2221 agttcttcta caagttcaac tgataagtca gatggggatt acggggaagg gaaaggtcag
2281 acaaatgaaa ttaatgcctt ggtacaattg atgactcaga cctgaaact ggattctaaa
2341 gagagctgtg aagatgtccc ggtagcaaac ccagtgtcag aattcaaaact tcatcggaaa
2401 tatcgggaca cactgatact tcatgggaag gttgcagaag aggcagagga aatccatttt
2461 aaagagctac cttcagctat tatgccaggt tctgaaaaga tcaggagact agttgaagtc
2521 ttgagaactg atgtaattcg tggcctggga gttcagcttt tagagcaggt gtatgatctt
2581 ttggaggagg aggatgaatt tgatagagag gtacgtttgc gggagcacat gggtgaaaag
2641 tatacaactt acagtgtgaa agctcgccag ttgaaatttt ttgaagaaaa catgaatttt
2701 tgagcatttg tcctaactcg ctgccagaat taaagacctt tttttagagg attttggtct
2761 aaaaagcaag ggcaaacagt catttggaag ccactcacca ctgttttata tctctttttt
2821 atatctcttt gccgtttccc tacagaaaaa aaattggaca gaacagaata atatgaagca
2881 ggatcacaaa agaaaaaaaaa ctttggtctt catattctct ttgtgaggag aaatctgttg
2941 tttgtttgat tactgtttac tgagccttaa tccaccaagt ttatatttag aatttttata
3001 ttttaaggta ctaattaaact taaacacaga gctataaaat gctggattga aaattttata
3061 ttgtaatgta gagataaaag cagtaggaga aacaaatgac ataatatgtc gtcataattc
3121 ctgctattgt taataacctt aaggagtagt tgataaatta taaaatttta aaaagtcaat
3181 tcagttctag aaatagattt aaagaatatg aagttctatc tagtacttga gcagctgtat
```



Figure 16  
Page 2 of 2

```
3241 ttcttttcta cacattgatg gacttttaaat attttatttct catttaatat aaacctcatc
3301 tagggatatat acaaattaaa actgagacac attggctttg taaatcagta tgtttttaca
3361 taatgggtttt gttagatttta tttttccatc agtgaaaaca tttcttaagc acaaatttca
3421 ttcccattta agcaatttgt aagcaaagtc caggtcatt tagtttttg atatatataa
3481 tgtttgctct ctgaagtttg tcttcagtga ctgtaagata ttagttgtct ttccatgttt
3541 taaatgtatg attatatagc acatatttta ttagttgttt aataagaggt aataccatc
3601 taggaaagaa attttatgaa gttaaataga agtcttgaat agtacatttt cacttctgta
3661 ttcgagggac tctaaaaata aatattgtct cagaaa
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SEQ ID NO:32  
Size: 841  
PRT STK2 (NEK4)

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1 MPLAAYCYLR VVGKGSYGEV TLVKHRRDGK QYVIKKLNLN NASSRERRAA EQEAQLLSQL
61 KHPNIVTYKE SWEGGDGLLY IVMGFCEGGD LYRKLKEQKG QLLPENQVVE WFWQIAMALQ
121 YLHEKHILHR DLKTQNVFLT RTNIIKVGDL GIARVLENHC DMASTLIGTP YYMSPELFSN
181 KPYNYKSDVW ALGCCVYEMA TLKHAFNAKD MNSLVYRIIE GKLPPMPRDY SPELAELIRT
241 MLSKRPEERP SVRSILRQPY IKRQISFFLE ATKIKTSKNN IKNGDSQSKP FATVVSGEAE
301 SNHEVIHPQP LSSEGSQTYI MGEKGCLSQE KPRASGLLKS PASLKAHTCK QDLSNTTELA
361 TISSVNIDIL PAKGRDSVSD GFVQENQPRY LDASNELGGI CSISQVEEEM LQDNTKSSAQ
421 PENLIPMWSS DIVTGEKNEP VKPLQPLIKE QKPKDQSLAL SPKLECSGTI LAHSNLRLLG
481 SSDSPASASR VAGITGVCHH AQDQVAGECI IEKQGRIHPD LQPHNSGSEP SLSRQRRQKR
541 REQTEHRGEK RQVRRDLFAF QESPPRFLPS HPIVGKVDVT STQKEAENQR RVVTGSVSSS
601 RSSEMSSSKD RPLSARERRR LKQSQEEMSS SGPSVRKASL SVAGPGKPQE EDQPLPARRL
661 SSDCSVTQER KQIHCLSEDE LSSSTSSTDK SDGDYGEKG QTNEINALVQ LMTQTLKLDS
721 KESCEDVPVA NPVSEFKLHR KYRDTLILHG KVAEEAEEIH FKELPSAIMP GSEKIRRLVE
781 VLRTDVIRGL GVQLLEQVYD LLEEDEFDR EVRLREHMGE KYTTYSVKAR QLKFFEENMN
841 F
```

Figure 17

SEQ ID NO:33  
Size: 1513  
DNA NKIAMRE

```

1 atggagatgt atgaaaccct tggaaaagtg ggagagggaa gttacggaac agtcatgaaa
61 tgtaaacata agaatactgg gcagatagtg gccattaaga tattttatga gagaccagaa
121 caatctgtca acaaaattgc gatgagagaa ataaagtttc taaagcaatt tcatcacgaa
181 aacctgggtca atctgattga agtttttaga cagaaaaaga aaattcattt ggtatttgaa
241 tttattgacc acacagtatt agatgagtta caacattatt gtcatggact agagagtaag
301 cgacttagaa aatacctctt ccagatcctt cgagcaattg actatcttca cagtaataat
361 atcattcatc gagatataaa acctgagaat attttagtat ccagtcagg aattactaag
421 ctctgtgatt ttggttttgc acgaacacta gcagctcctg gggacattta tacggactat
481 gtggccacac gctggtatag agctcccgaa ttagtattaa aagatacttc ttatggaaaa
541 cctgtggata tctgggcttt gggctgtatg atcattgaga tggccactgg aaatccctat
601 cttcctagta gttctgattt ggatttactc cataaaattg ttttgaaagt gggcaatttg
661 tcacctcact tgcagaatat cttttccaag agccccattt ttgctggggg agttcttctt
721 caagttcaac accccaaaaa tgcaagaaaa aaatatccaa agcttaatgg attgttggca
781 gatatagttc atgcttgttt acaaattgat cctgctgaca ggatatcatc tagtgcctt
841 ttgcatcatg agtattttac tagagatgga tttattgaaa aattcatgcc agaactgaaa
901 gctaaattac tgcaggaagc aaaagtcaat tcattaataa agcāaaaaga gagttctaaa
961 gaaaatgaac tcaggaaaga tgaaagaaaa acagtttata ccaatacact gctaagtagt
1021 tcagtttttg gagaggaaat agaaaaagag aaaaagccca aggagatcaa agtcagagtt
1081 attaaagtca aaggaggaag aggagatatc tcagaaccaa aaaagaaaga gtatgaaggt
1141 ggacttggtc aacaggatgc aaatgaaaat gttcatccta tgtctccaga tacaaaactt
1201 gtaaccattg aaccacaaaa ccctatcaat cccagcacta actgtaatgg cttgaaagaa
1261 aatccacatt gcggagggtc tgtaacaatg ccacccatca atctaactaa cagtaatttg
1321 atggctgcaa atctcagttc aaatctcttt caccctcagt tgagggtgagc tgtaacagag
1381 aagaaaccta aataatacaa cattcctgta taatggtatt tcaaagaatc gtgttcatag
1441 tgtctgtatg taaactgaac ttgaagaaaa tatattgaaa ttaaagctgt ataatgggcc
1501 aaaaaaaaaa aaa

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SEQ ID NO:34  
Size: 455  
PRT NKIAMRE

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1 MEMYETLGKV GEGSYGTVMK CKHKNTGQIV AIKIFYERPE QSVNKIAMRE IKFLKQFHHE
61 NLVNLIEVFR QKKKIHLVFE FIDHTVLDEL QHYCHGLESK RLRKYLQIL RAIDYLSNN
121 IHRDIKPEN ILVSQSGITK LCDFGFARTL AAPGDIYTDY VATRWYRAPE LVLKDTSYGK
181 PVDI WALGCM I IEMATGNPY LPSSSDL DLL HKIVLKVGNL SPHLQNI FSK SPIFAGV VLP
241 QVQHPKNARK KYPKLNGLLA DIVHACLQID PADRISSDL LHHEYFTRDG FIEKFMP ELK
301 AKLLQEAKVN SLIKPKESSK ENELRKDERK TVYTNLLSS SVLGEEIEKE KKPKEIKVRV
361 IKVKGGRGDI SEPKKKEYEG GLGQQDANEN VHPMSPDTKL VTIEPPNPIN PSTNCNGLKE
421 NPHCGGSVTM PPINLTNSNL MAANLSSNLF HPSVR

```

Figure 18  
Page 1 of 2

SEQ ID NO:35  
Size: 3504  
DNA HBO1

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1 gccgctgccc gaatcggaac cgtcggggccg cagccgccgg caatgccgcg aaggaagagg
61 aatgcaggca gtagttcaga tggaaaccgaa gattccgatt tttctacaga tctcgagcac
121 acagacagtt cagaaagtga tggcacatcc cgacgatctg ctcgagtcac ccgctcctca
181 gccaggctaa gccagagttc tcaagattcc agtcctgttc gaaatctgca gtcttttggc
241 actgaggagc ctgcttactc taccagaaga gtgaccgcta gtcagcagca gcctacccca
301 gtgacaccga aaaaatacc ctttcggcag actcgttcat ctggttcaga aactgagcaa
361 gtggttgatt tttcagatag agaaactaaa aatacagctg atcatgatga gtcaccgcct
421 cgaactccaa ctggaaatgc gccttcttct gagtctgaca tagatatctc cagccccaat
481 gtatctcacg atgagagcat tgccaaggac atgtccctga aggactcagg cagtgatctc
541 tctcatcgcc ccaagcgccg tcgcttccat gaaagctaca acttcaatat gaagtgtcct
601 acaccaggct gtaactctct aggacacctt acaggaaaac atgagagaca tttctccatc
661 tcaggatgcc cactgtatca taacctctca gctgacgaat gcaagggtgag agcacagagc
721 cgggataagc agatagaaga aaggatgctg tctcacaggc aagatgacaa caacaggcat
781 gcaaccaggc accaggcacc aacggagagg cagcttcgat ataaggaaaa agtggctgaa
841 ctcaggaaga aaagaaattc tggactgagc aaagaacaga aagagaaata tatggaacac
901 agacagacct atgggaacac acgggaacct cttttagaaa acctgacaag cgagtatgac
961 ttggatcttt tccgaagagc acaagcccgg gcttcagagg atttggagaa gtttaaggctg
1021 caaggccaaa tcacagaggg aagcaacatg attaaaaaa ttgcttttgg ccgctatgag
1081 cttgatacct ggtatcattc tccatatect gaagaatatg cacggctggg acgtctctat
1141 atgtgtgaat tctgtttaaa atatatgaag agccaaacga tactccgccg gcacatggcc
1201 aaatgtgtgt ggaaacaccc acctggtgat gagatatatc gcaaagggtc aatctctgtg
1261 tttgaagtgg atggcaagaa aaacaagatc tactgcaaaa acctgtgcct gttggccaaa
1321 ctttttctgg accacaagac attatattat gatgtggagc ctttctgtt ctatgttatg
1381 acagggcgg acaacactgg ctgtcacctt attggatatt tttctaagga aaagaattca
1441 tccctcaact acaacgtctc ctgtatcctt actatgcctc agttagctat acaggctctat
1501 ggcaagatgc ttattgattt cagttatttg ctttccaaag tcgaagaaaa agttggctcc
1561 ccagaacgtc cactctcaga tctggggctt ataagctatc gcagttactg gaaagaagta
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1681 gagacggctg tgaatcctgt ggacattgtc agcactctgc aagcccttca gatgctcaaa
1741 tactggaagg gaaaacacct agttttaaag agacaggacc tgattgatga gtggatagcc
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1921 tccgtaccct agggatctgt ctgtcatttc tctgttgctc ttgtgattgg aagtagcagt
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2041 agacgtggt tctgaggaac tgttgtttcg gcctcagtga ggttgccctg atgggatctg
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2161 cctgtccagt cactggttct ctctcatgt cctctcgccc catgaggttg tgttgtgtct
2221 tctaagcgtg gtactagtgc ttgccacctg gtcaccagac ctccaaatat ggctgccacc
2281 accaggacct ttccagttac tccttatatg tgtgttctat ggaggggcag ggaaaagggtg
2341 gcacttgtga gtgtgtgtgg attggcaggg ggtccattca ctttgggttc catcttgctt
2401 taaatttctt cattttgatt aagagacctc tttttgatct gtattgggct aaccagagcc
2461 aaatactttt gaagagtttc ccagggaacta gtcattggtaa tagcatataa ttgatctgaa
2521 tgagatggag agaagaatga aggggtgggt gttctgggtt tgatttgagt tcacctgtgg
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2761 agaaaccttt tcacctccac tagtctgata cagtacatct gtacttccat ataccttgca
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3121 ttggggcaac ttttgatgta tgacatgtca ccttcccaa cttggtctcc tccaacatgc
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Figure 18  
Page 2 of 2

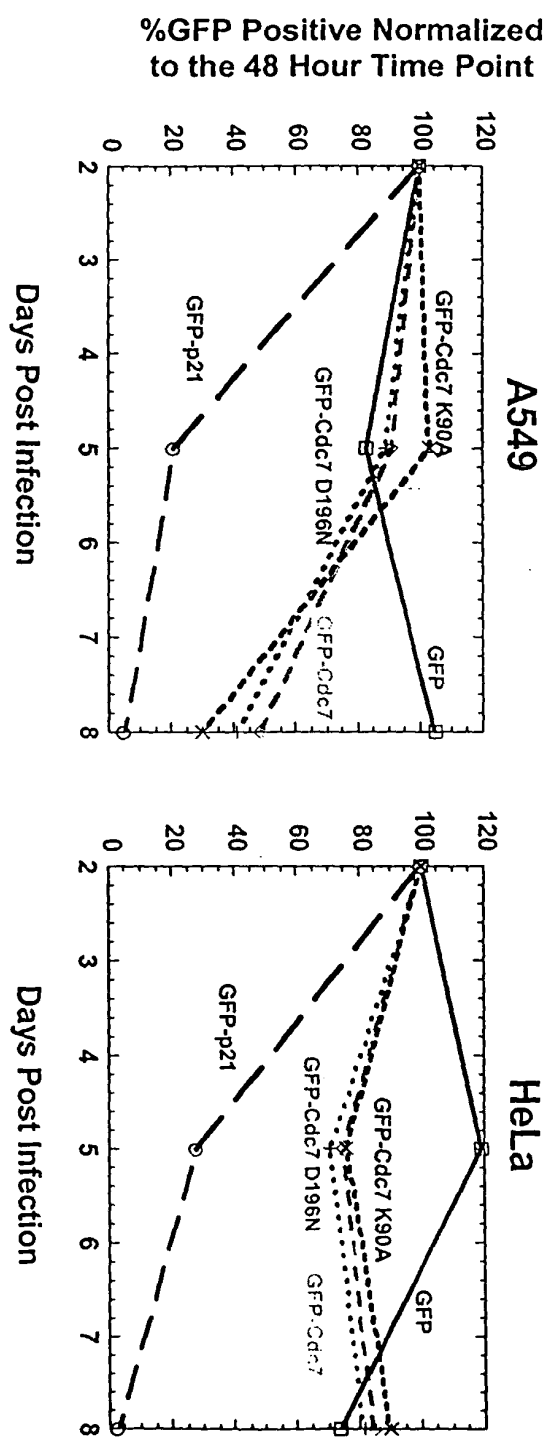
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3361 taggggtttt cttaagggat aaaggccttt tacagaagct aaacccttcc ccacatgtgg
3421 tagaatgtgc tcttctatat ctactctca ataaagcatg ttctctgctc aaaaaaaaaa
3481 aaaaaaaaaa aaaaaaaaaa aaaa
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SEQ ID NO:36  
Size: 611  
PRT HBO1

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1  MPRRKRNAGS SSDGTEDSDF STDLEHTDSS ESDGTSRRSA RVTRSSARLS QSSQDSSPVR
61  NLQSFQTEEP AYSTRRVTRS QQQPTPVTPK KYPLRQTRSS GSETEQVVDF SDRETKNTAD
121 HDESPRPTPT GNAPSSSEDI DISSPNVSHD ESIKDMSLK DSGSDLSHRP KRRRFHESYN
181 FNMKCPTPGC NSLGHLTGKH ERHFSISGCP LYHNLSADEC KVRAQSRDKQ IEERMLSHRQ
241 DDNNRHATRH QAPTERQLRY KEKVAELRKK RNSGLSKEQK EKMEHRQTY GNTREPLEN
301 LTSEYDLDLF RRAQARASED LEKLRLQGQI TEGSNMIKTI AFGRYELDTW YHSPYPEEYA
361 RLGRLYMCEF CLKYMKSQTI LRRHMAKCVW KHPPGDEIYR KGSISVFEVD GKKNKIYCQN
421 LCLLAKLFLD HKTLYYDVEP FLFYVMTEAD NTGCHLIGYF SKEKNSFLNY NVSCILTMPQ
481 YMRQGYGKML IDFSYLLSKV EEKVGSPERP LSDLGLISYR SYWKEVLLRY LHNFGQKEIS
541 IKEISQETAV NPVDIVSTLQ ALQMLKYWKG KHLVLKRQDL IDEWIAKEAK RSNSNKTMDP
601 SCLKWTPPKG T
```

Gene Name	Accession (nt/aa)	Screen	Activity
PKC-zeta	NM_002744/AAA36488	ATM ip	S/T kinase
PLC-beta 1	NM_01519/NP_056007	RbAp48 ip	Phospholipase
PTK2(FAK)	L05186/AAA35819	14-3-3 YTH	Y kinase
PTK2b(FAK2)	L49207/Q14289	XIAP YTH	Y kinase
CK2	NM_001895/NP_001886	DNAPK YTH	S/T kinase
cMET	J02958/AAA59591	RbAp48 ip	Y kinase
FEN1	NM_004111/NP_004102	PCNA YTH	Endonuclease
REV1	AF206019/AAF18986	Myt1 YTH	dCMP transferase
APE1:	X66133/S34422	p16 YTH	Endonuclease
CDK3:	NM_001258/NP_001249	CKS2, HSPC YTH	S/T kinase
PIM1	M16750/AAA60089	p21 ip	S/T kinase
CDC7L1	NM_003503/NP_003494	Apoptin, GADD34 YTH + bioinf	S/T kinase
CDK7	NM_001799/NP_001790	CIP1 YTH+bioinf	S/T kinase
CNK	NM_004073/NP_004064	DNAPKF7 YTH	S/T kinase
PRL-3	NM_007079/NP_009010	Myt1 YTH	Y phosphatase
STK2	XM_003216/XP_003216	p73 YTH	S/T kinase
NKIAMRE	AF130372/AAF36509	RbAp48 ip	S/T kinase.
HBO1	NM_007067/NP_008998	p66H YTH	Histon acetylase

FIGURE 19



<u>%GFP Positive at 48 Hours</u>	
<u>A549</u>	<u>HeLa</u>
● GFP-p21	7.1
□ GFP	31.5
◇ GFP-Cdc7	1.27
× GFP-Cdc7 K90A	0.82
+ GFP-Cdc7 D196N	1.12

FIGURE 20

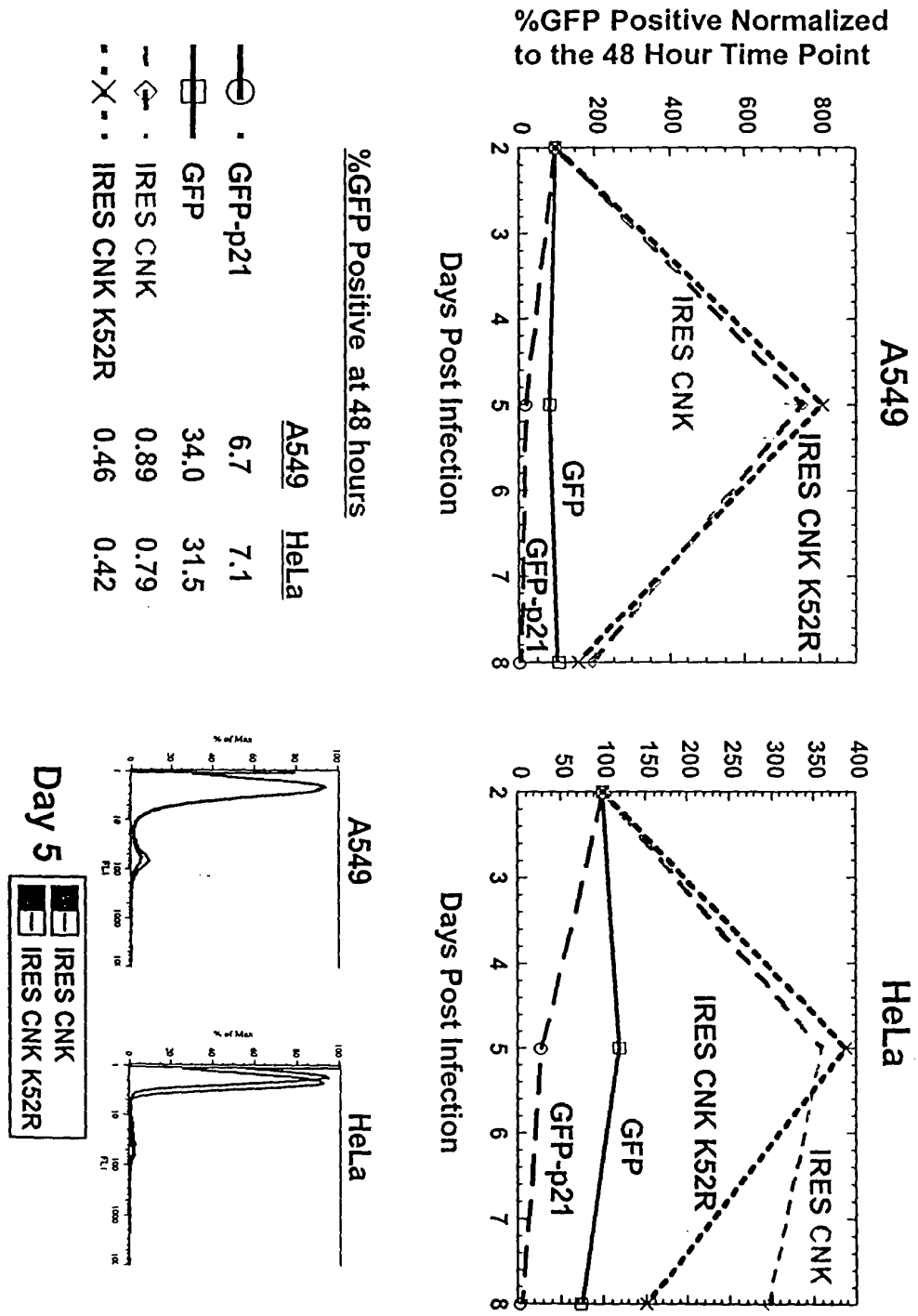
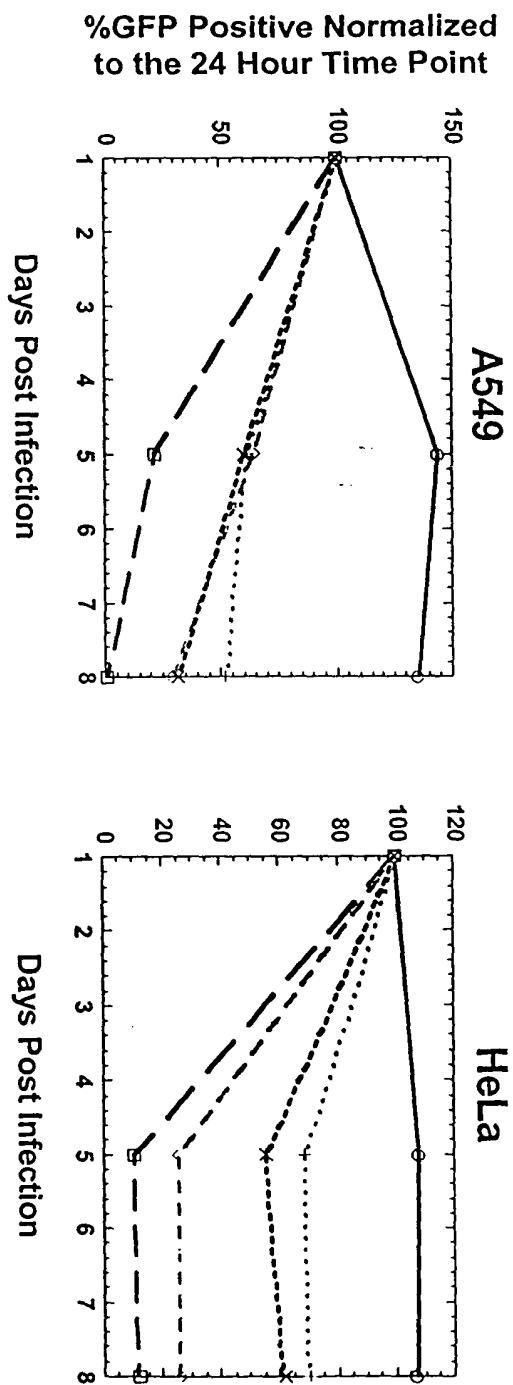


FIGURE 21



%GFP Positive at 24 Hours

	A549	HeLa
—■— GFP	52.8	59.0
—●— GFP-p21	11.0	23.1
—◇— GFP-STK2S	9.99	9.65
—×— GFP-STK2S K35A	9.23	7.88
···+··· GFP-STK2S D149A	7.35	6.56

FIGURE 22



Point mutant : K90A, D196N - K90A corresponds to a mutation in the catalytic residue in the kinase domain  
D196N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

CDC7L1	MEASLGIMDEPMAFSPQRDRFQAEGLKKNQNFKLAGVKKDIEKL YEAVPOLSNVFKI
CDC7Sc	-----MTSKTKNIDIPPEIKEEMIQLYHDLPGIENEYKL
	: * : : * : : * : * : *
	: : : : * : : * : * : *
CDC7L1	EDKIGEGTFSSVYLAT-----AQLQVPEEKALKHLPTSHPIRIAAELQCLT
CDC7Sc	IDKIGEGTFSSVYKAKDITGKTKKFASHFWNYSNVYALKKIYVTSPPQRIYNELNLLY
	***** * : : : * : * : *
	: : : * : * : * : * : *
CDC7L1	VAGGQDNVMGVKCYCFRKNQDVVIAMPYLEHESFLDILNSLSQAEVREYMLNLFKALKRIH
CDC7Sc	IMTGSSRVAPLCDAKVRDQVIAVLPYPHEEFRTFYRDLPPIGIIKKYIWELLRALKFVH
	: * : : * : * : * : * : *
	: : : : * : : * : * : *
CDC7L1	QFGIVHRDVKPSNFLYNRRLKKYALVDFGLAAGTHDTKIELLKVFQSEAAQDERCSQNKSH
CDC7Sc	SKGIIHRDIKPTNLFNLELGRGVLVDFGLAEAQMDYKSMISSQND-----
	***** * : : * : *
	: : : * : * : * : *
CDC7L1	IITGNKIPLSGVPVKELDQAQSTTKASVKRPYTNAQIAIKQKGKESVGLSVQRSVFGE
CDC7Sc	-----YDN-----YANTNHDGGYSMRNHEQFCPC
	: : : * : * : * : *
	: : : * : * : * : *
CDC7L1	RNFNIHSSISHESPAVKLMKQSKTVLDLSRKLATKKKAISTKYMNSAVMRKTASSCPASL
CDC7Sc	IMRNQYSPNSHNQTPMVTIQNGKVHLN-----
	* : * : * : * : *
	: : : : * : : * : * : *
CDC7L1	TCDCYATDKVCSICLSRQQAVAPRAGTGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLS
CDC7Sc	NVNGVDLTKGYPKNETRIKIRANRAGTRGFRAPVLMKCGAASKIDIWVSGVILLSLG
	: : * : * : * : * : *
	: : * : * : * : * : *

FIGURE 23

Point mutant : K52R and D146A - the catalytic residue in the kinase domain.  
(J. Biol. Chem., Vol. 276, Issue 46, 43305-43312, November 16, 2001. PMID: 11551930)

kinase: domain 1 of 1, from 23 to 275: score 309.5, E = 2.5e-90

```

*->yelleklGegsfGkvYkakhkdktgkivAvKilLkkekesikek...r
Y +++ lG+G+f+++y+++ +tg +AvK+++ + + k+++++
Y LKGRLLGKGGFARCYEATDT-ETGSAYAVKVIP-QSRVAKPHqrek 67

query 23 YLKGRLGKGGFARCYEATDT-ETGSAYAVKVIP-QSRVAKPHqrek 67

flreiqlkrlshpNivrligvfedtdhlylvmEymegDlfdylrrng
+l+Ei++++ L+H +Ivr+ + fe + d+++y+ +E++ +L+++++++
68 I LNEIELHRDLQHRHIVRFSHFEE-DADNITYIFLELCSRKSLAHlWKARH 116

query 68 I LNEIELHRDLQHRHIVRFSHFEE-DADNITYIFLELCSRKSLAHlWKARH 116

gplsekeakkialQilrgleYlHsngivHRDLKpENllLdendgtvKiaD
+ l e+++ + +Qil+Gl+YlH +gi+HRDLK N++++en + +K++D
117 TLL-EPEVRYYLrQILSGELKYLHQRGILHRDLKLGNFfITEN-MELKVGD 164

query 117 TLL-EPEVRYYLrQILSGELKYLHQRGILHRDLKLGNFfITEN-MELKVGD 164

FGLARlle.ssskltttfvGTPwYmmAPEvilegrgysskvDvWSlGvily
FGLA+ le++ ++++t++GTP+Y+ APEv l+++g+++++DvWSlG+++Y
165 FGLARLEpPEQRKKTICGTPNVV-APEV-LLRQGHGPEADVWSlGCVMY 212

query 165 FGLARLEpPEQRKKTICGTPNVV-APEV-LLRQGHGPEADVWSlGCVMY 212

ElItgspIfpgadlpafTgdevdqliifvklpfsdelpKtridpleel
ll+g +Pf+ + l+e
213 TLlCG-----SPPFE-----TADLKET 229

query 213 TLlCG-----SPPFE-----TADLKET 229

friikrpglrIpIpsncSeelkdlLkclnKDpskRpGsatakeilnhpwf
+r ik+ ++ lp ++S ++++Ll +L+ P +Rp ++ +il h +f
230 YRCIKQ--VHYTLPASLSLPARQLLAAlLRASPRDRP---SIDQILRHDFf 275

query 230 YRCIKQ--VHYTLPASLSLPARQLLAAlLRASPRDRP---SIDQILRHDFf 275

```

FIGURE 24

Point mutants : K35A and D149A - the catalytic residue in the kinase domain.

kinase: domain 1 of 1, from 6 to 261: score 288.9, E = 4.2e-84  
 \*->yel1ek1GegsfGkykakhkdtgkiVAvkilkkikesiek...r  
 Y 1+++G+Gs+G+V ++kh+ +gk+++K+1+ ++ ++++++  
 query 6 YCYLRVVGKGSYGVTLVKHR-RDGKQYVIKKLN--LRNASSRerTA 49

f1rEiqilkrLshpNivrligvfedtdhlylvmEymegGdlfdylrrng  
 + E+q+1 +L+HpNiv+++++e d+ ly+vm ++egGdl++ 1++++  
 query 50 AEQEAQLLSQLKHPNIVTYKESWEGDGLLYVMGFCEGDLYRKLKEQK 99

.gplsekeakkialQilrgleyLHsngivHRDLKpeNIlldendgtvkia  
 + 1+++++ ++ Qi+ +1+YLH+++i+HRDLK++N++1++ + +K++  
 query 100 GQLLPENQVWEVQIAMAALOYLHEKHILHRDLKTQNVFLTRT-NIIRVG 148

DFGLArlle.sssklttfvGTpwYmmaPEvilegrgysskVDwSlGvil  
 D G+Ar+le++ +++t+ GTP+Ym +PE+ ++++Y k+DvW+lg+ +  
 query 149 DLGIARVLEHCDMASTLIGTPYYM-SPEL-FSNKPYNYKSDVWALGCCV 196

YELLtgplfpgadlpafgtgdevdqliifvklpfsdelpktridplee  
 YE+++ k f +d+ +  
 query 197 YEMATL-----KHAFNA-----KDMNSL 214

lfriikrpglrlp1psncSeelkdl1kkclnkDpskrpGsatakeilnhpwf<-\*  
 ++rii++ ++p p+ S+el +L++ +L k P++Rp + + il p++  
 query 215 VYRIIEG--KLPMWRDYSPELAELIRTMLSKRPEERP---SVRSILRQPYI 261

FIGURE 25

# Dominant Negative Mutants for Cdc7L1

Point mutant : K90A, D196N - K90A corresponds to a mutation in the catalytic residue in the kinase domain  
D196N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

CDC7L1	MEASLGIQMDEPMAFSPQRDRFQAEGSLKXNEQNFKLQAGVKKDIEKLYEAVPQLSNVFKI
CDC7Sc	-----MTSKTKNIDDIPEIKEEMIQLYHDLPGIENEYKL
	: *::: : . : *::: : *::: : *::: : *::: : *
	○
CDC7L1	EDKIGEGTFSSVYLAT-----AQLQVGPEEKIALKHLIPTSHPIRIAAELQCLT
CDC7Sc	IDKIGEGTFSSVYKAKDITGKITKKFASHFWNGSNYVALKKIYVTSSPQRIYNELNLLY
	***** * .::: : *::: : *::: : *::: : *
CDC7L1	VAGGQDNVMGVKCYCFRKNHVVIAAMPYLEHESFLDIINLSFQEVREYMLNLFKALKRIH
CDC7Sc	IMTGSSRVAPLCDAKRVRDQVIAPLPYPPEEFRTFRDLPIKGIKKIYIWEILLRALKFVH
	: *... * : . * *::: : *::: : *::: : *::: : *::: : *
	○
CDC7L1	QFGIVHRDVKPSNFLYNRLKKYALVDFGLAQGTHDTKIELLKVFVQSEAQQERCSONKSH
CDC7Sc	SKGI IHRDIKPTNLFNLELGRGVLVDFGLAEAQMDYKSMISSQND-----
	. **::: **::: **::: * . * . *****::: . * * : . :
CDC7L1	IITGNKIPLSGVPKELDQQSTTKASVKRPTYTNAQIQKQKDGKESVGLSVQRSVFGE
CDC7Sc	-----YDN-----YANTNHDGGYSMRNHEQFCPC
	: . . . . . : . . . . . : . . . . . : . . . . .
CDC7L1	RNFNIHSSISHESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASL
CDC7Sc	IMRNQYSPNSHNQTPPMVTIQNGKVHLN-----
	* : * . *::: . . : * . * *
CDC7L1	TCDCYATDKVCSICLSRRQVAPRAGTGFRAPEVLTKPCNPQTATDMWSAGVIFLSLLS
CDC7Sc	NVANGVDLTGYPKNETRRIKRANRAGTRGFRAPVLKMKCAQSTKIDISVGVILLSLLG
	. : * . . : * * : * ***** * * * * *::: *::: *::: *::: *::: *

FIGURE 26

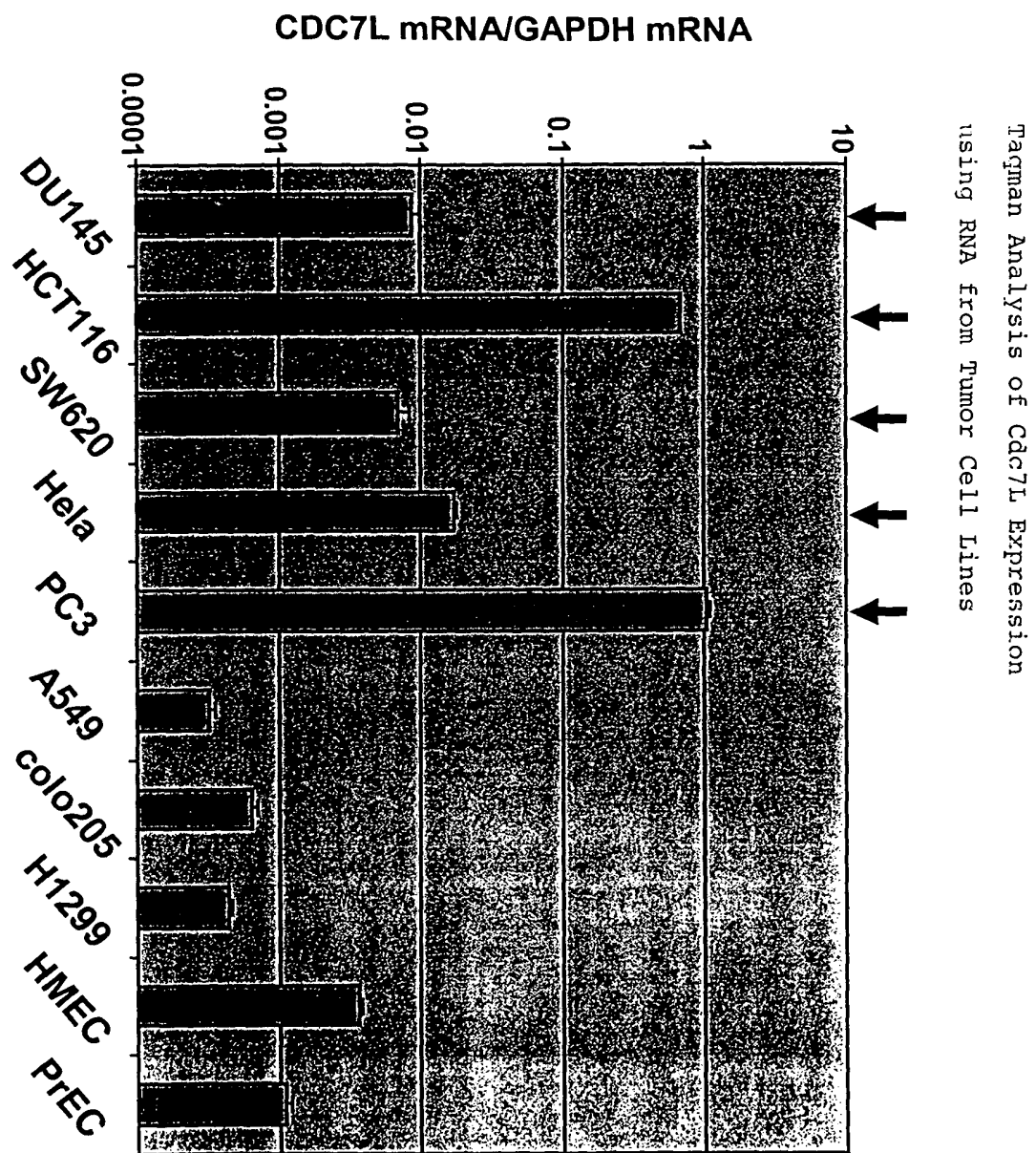


FIGURE 27

CDC7L mRNA Levels are Higher in Diseased Tissue  
 Relative to Normal Tissue in Patients with Lung Carcinomas

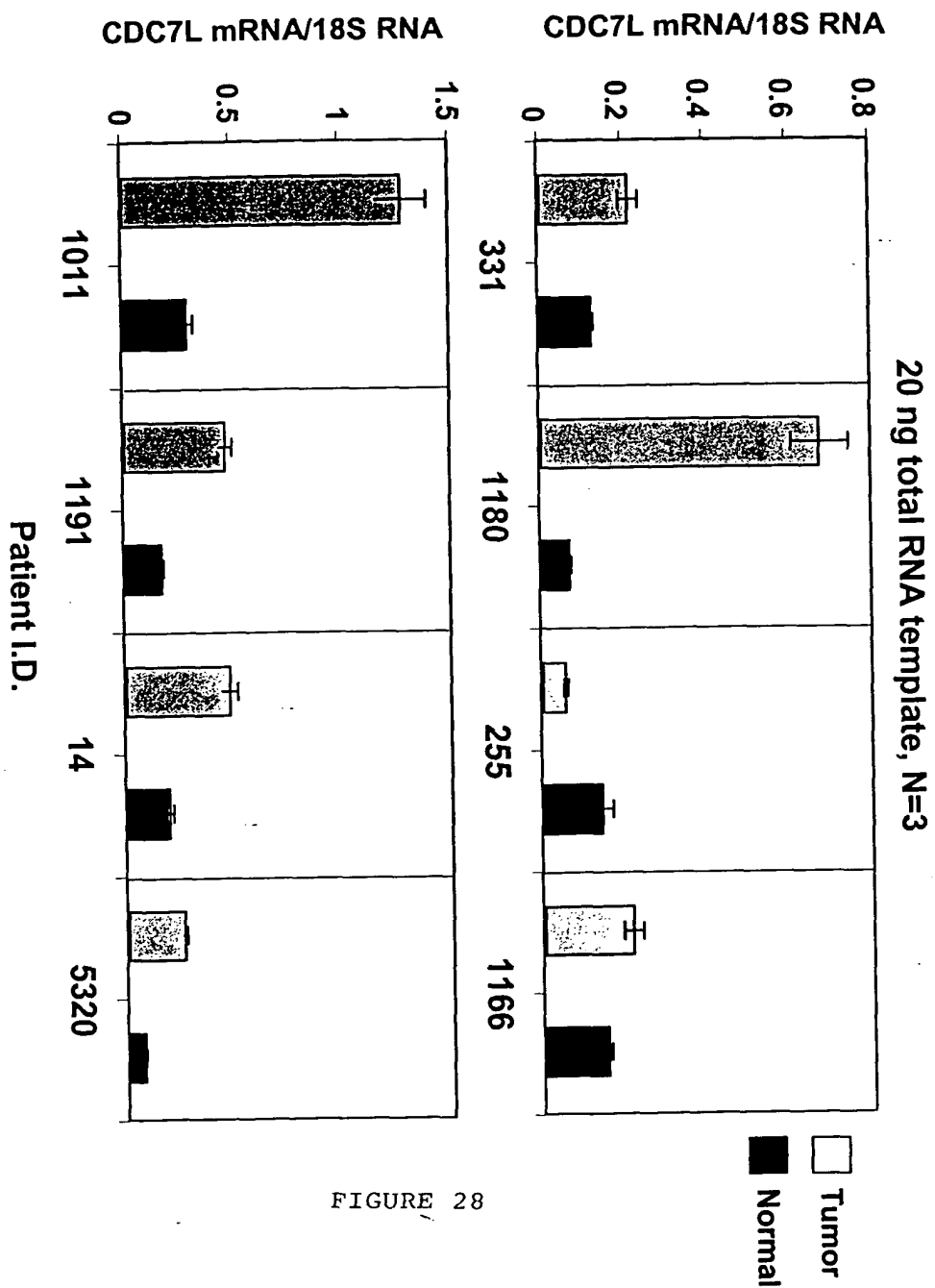


FIGURE 28

CDC7L mRNA Levels are Higher in Diseased Tissue  
 Relative to Normal Tissue in Patients with Colon Carcinoma

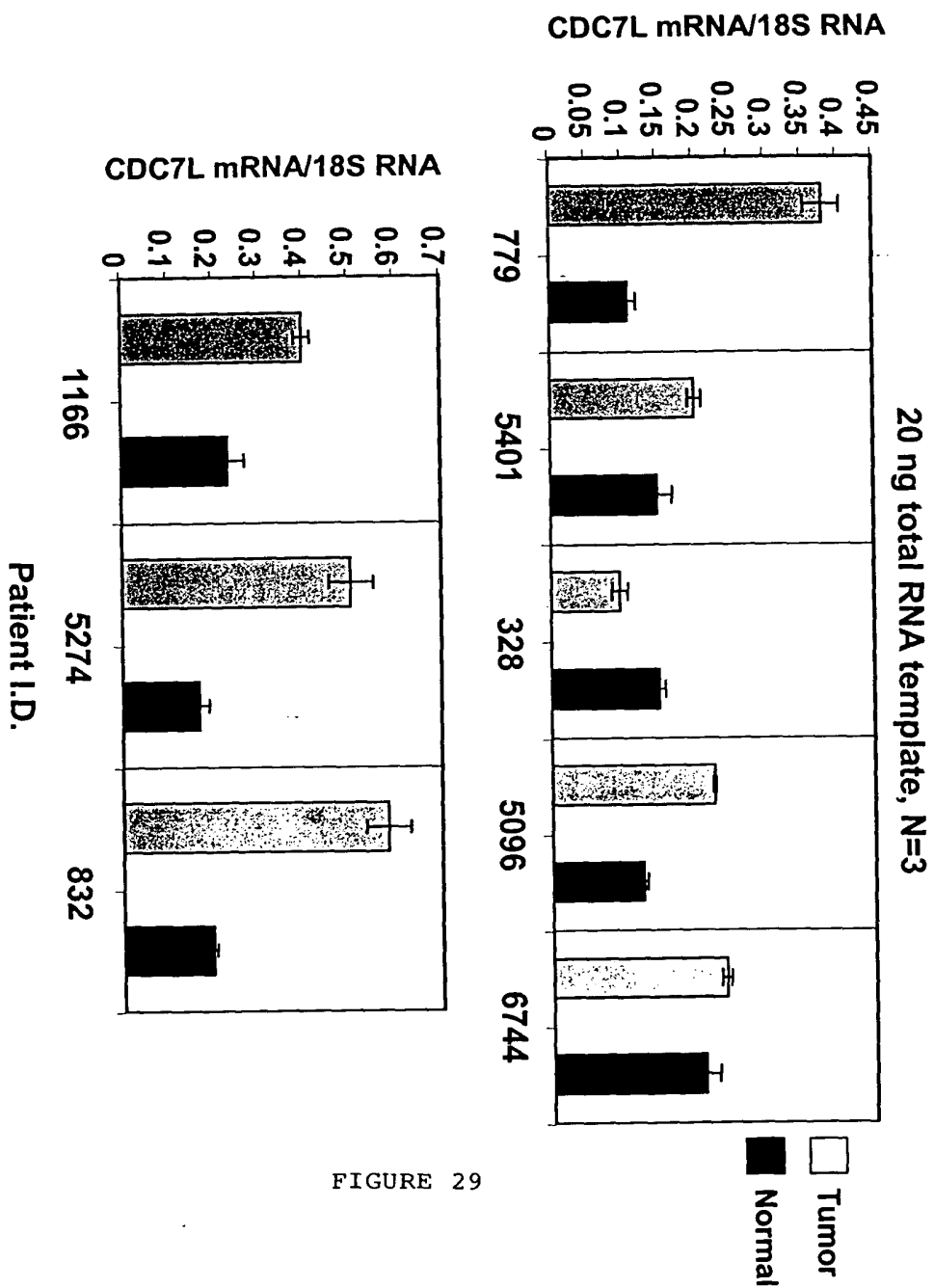


FIGURE 29

# **Taqman Analysis of CNK Expression Using RNA from Tumor Cell Lines**

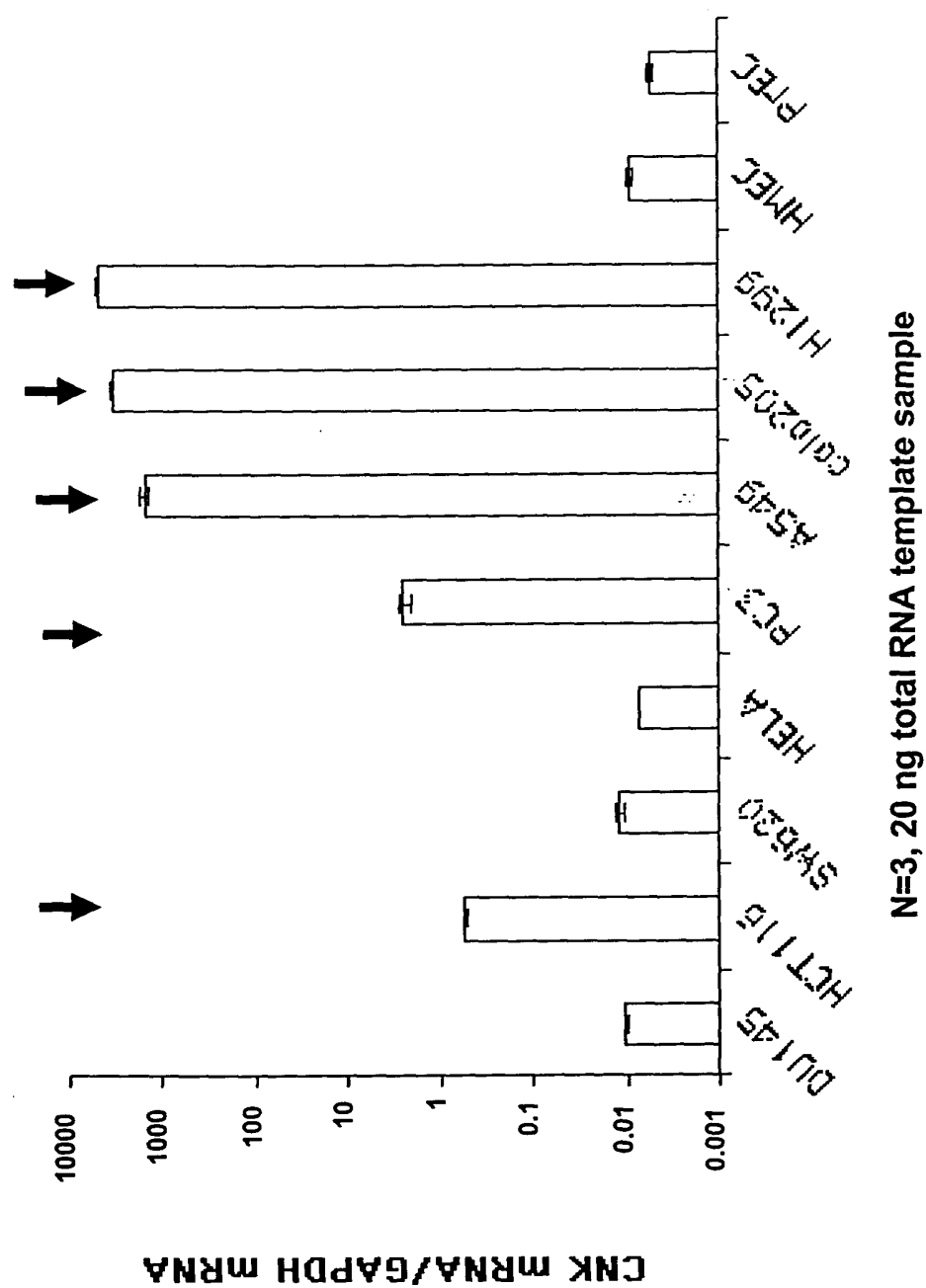


FIGURE 30



## 13



**Kinase reactions were performed for 30 minutes at R.T. using 2 clones of each construct.**

# RT-PCR of mRNAs From Different Tissues and Cell Lines Suggests that the Larger STK2 Isoform Predominates in *H. Sapiens*

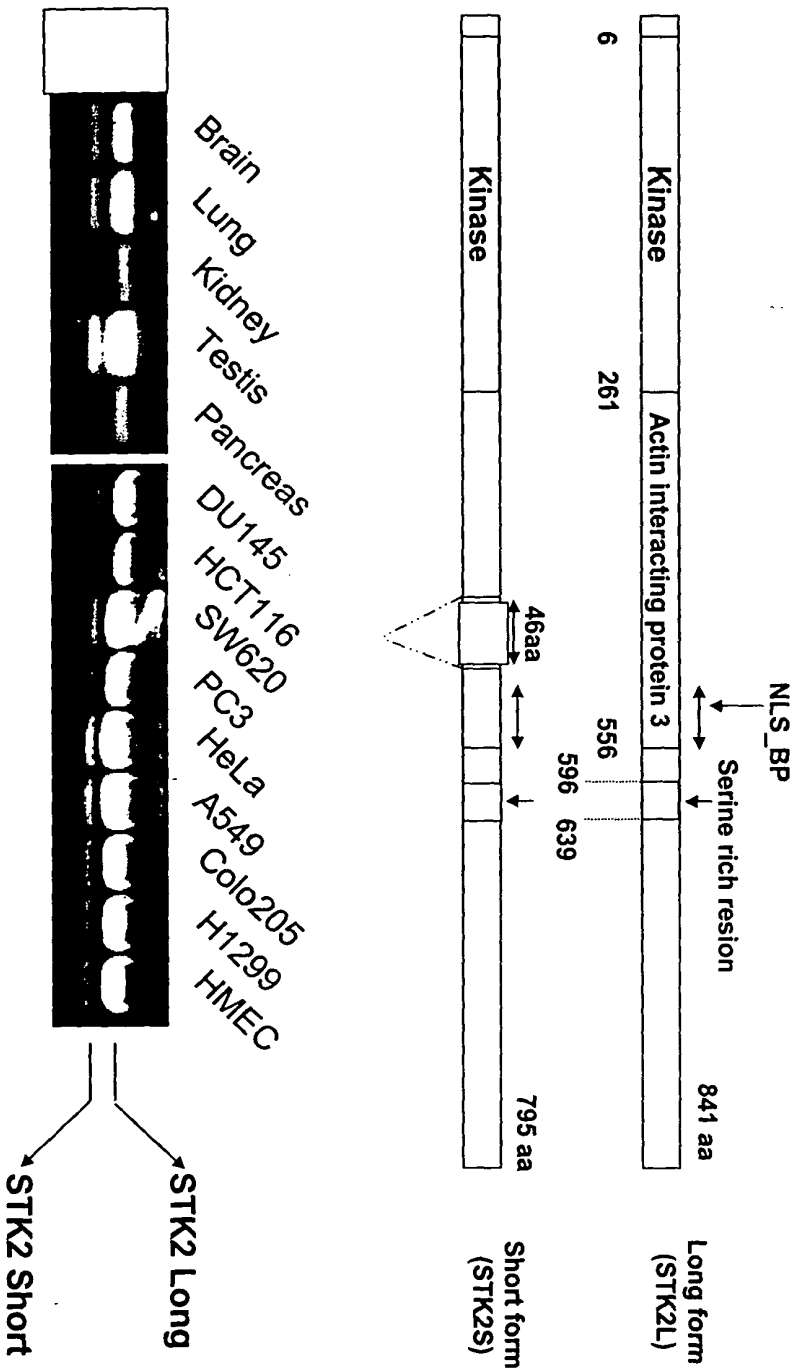
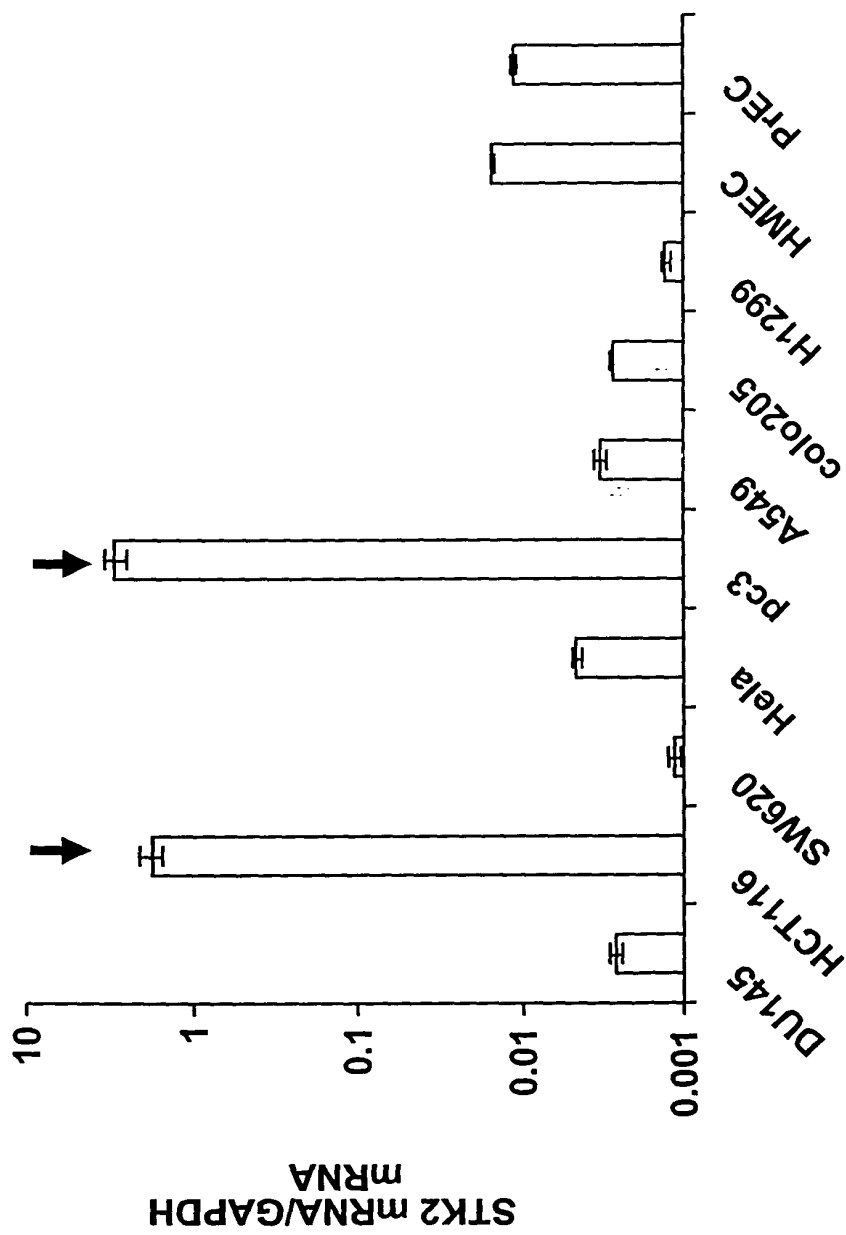


FIGURE 32

# **Taqman Analysis of STK2 Expression using RNA from Tumor Cell Lines**



N=3, 20 ng total RNA template sample

FIGURE 33

# GFP-STK2 Short is Antiproliferative when Measured Using the Cell Tracker Assay

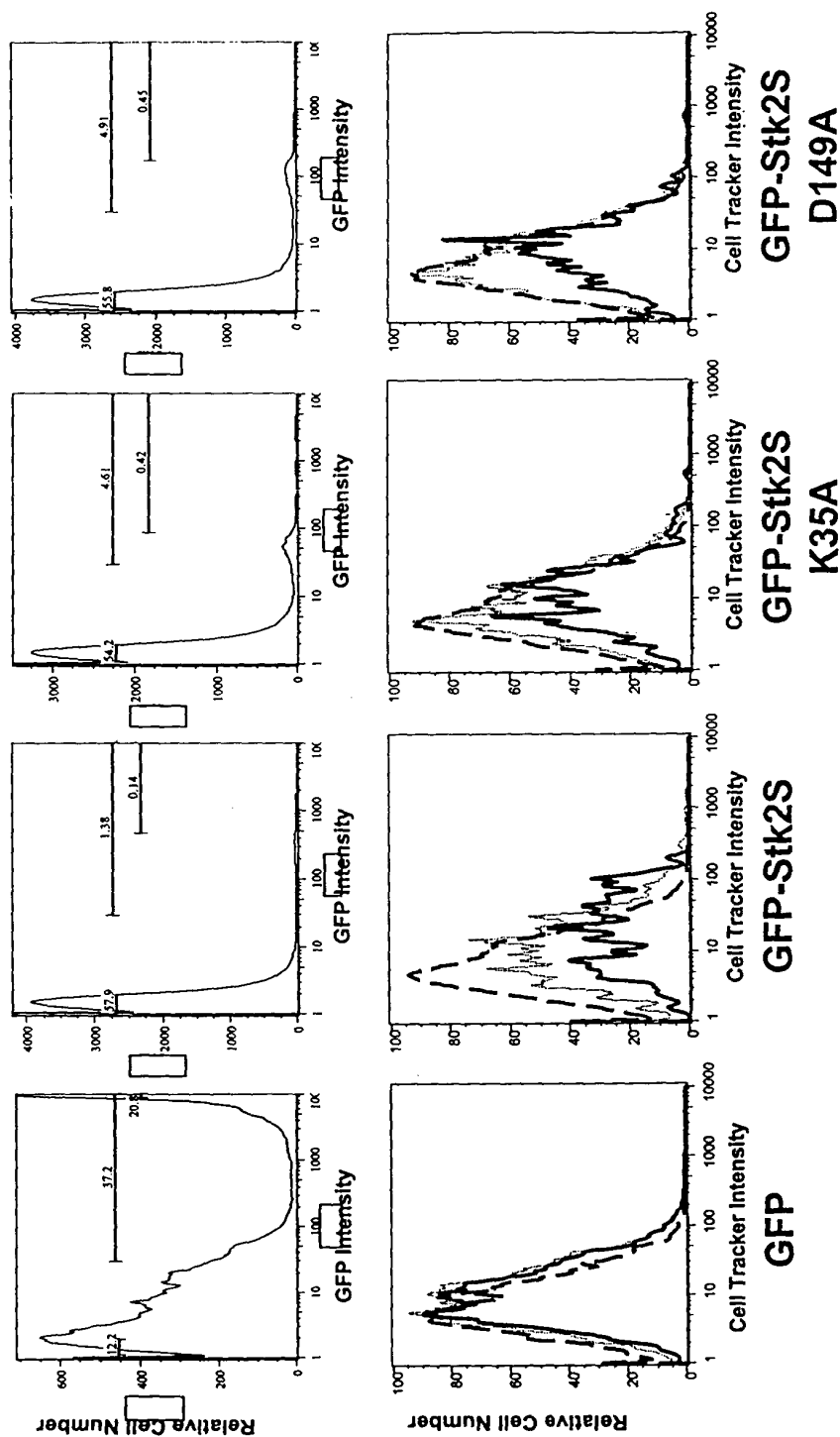


FIGURE 34

Cell Tracker Assay Day 8 A549 ..... GFP Pos. --- GFP Neg. — GFP Hi

# Expression of GFP-Stk2 Long is Antiproliferative in A549 and HeLa Cells

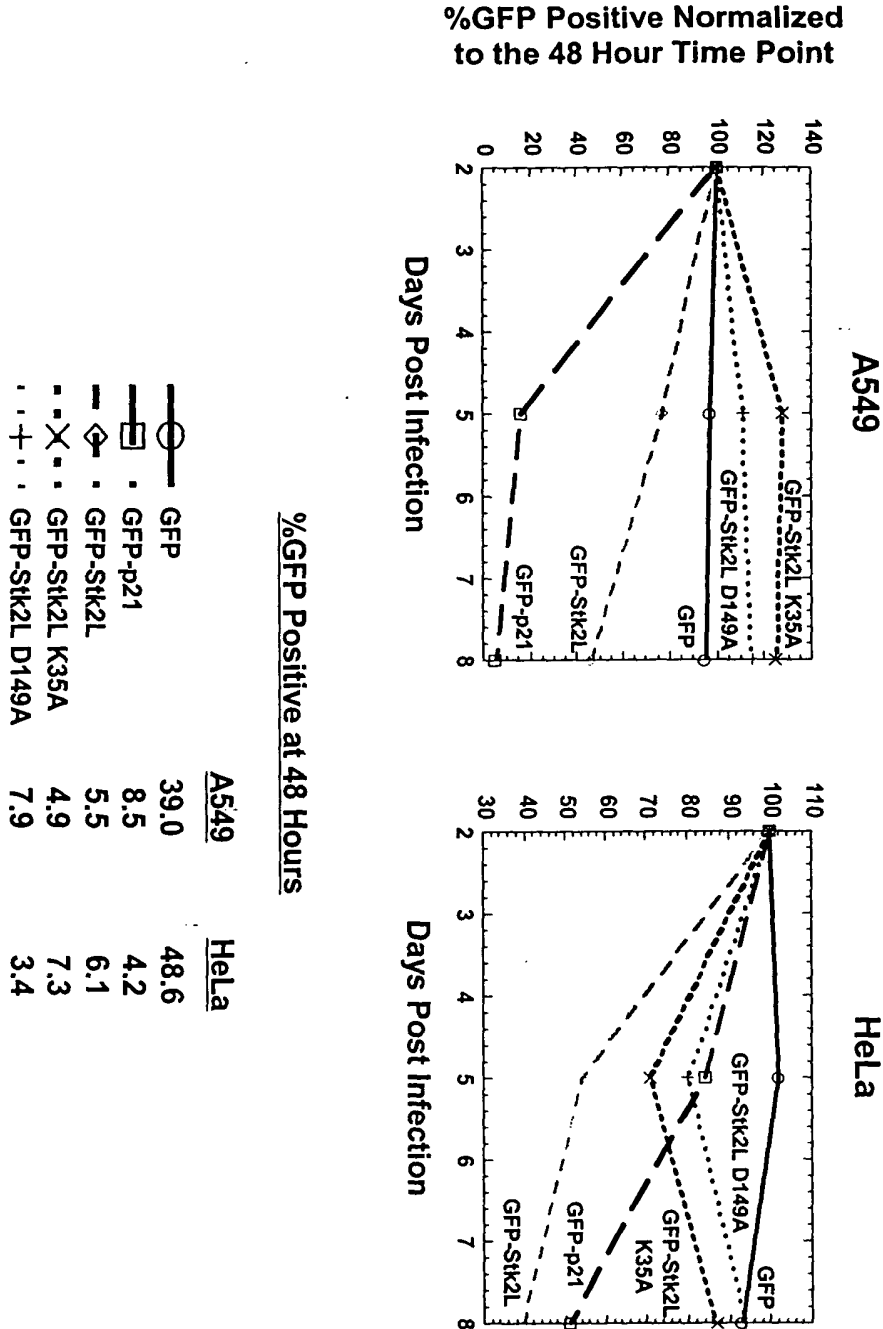


FIGURE 35

# GFP-STK2 Long is Antiproliferative when Measured Using the Cell Tracker Assay

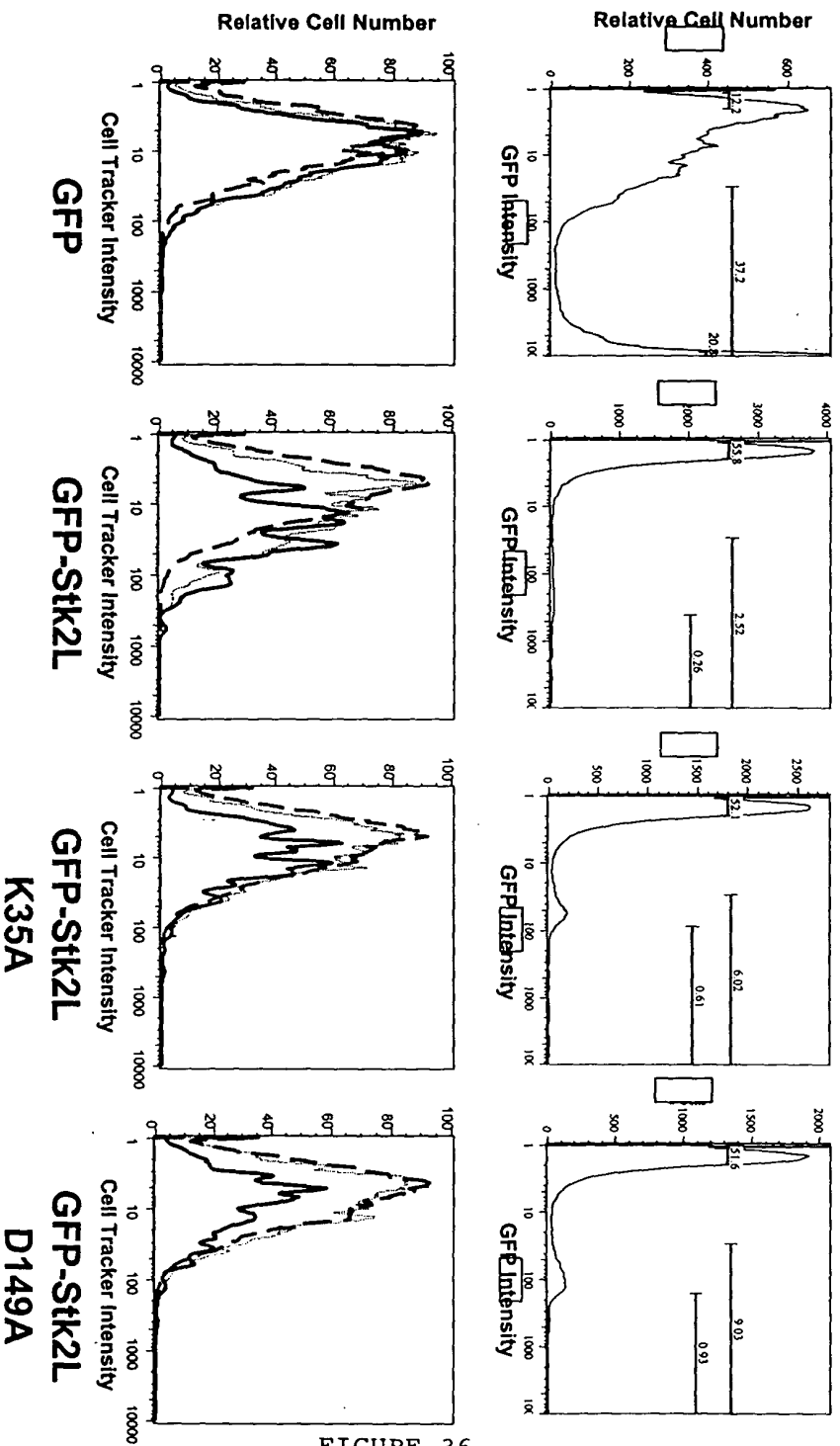


FIGURE 36

Cell Tracker Assay Day 8 A549 ..... GFP Pos. — GFP Neg. — GFP Hi

# Expression of STK2L WT and Mutants Using IRES Vectors is Antiproliferative in A549 Cells

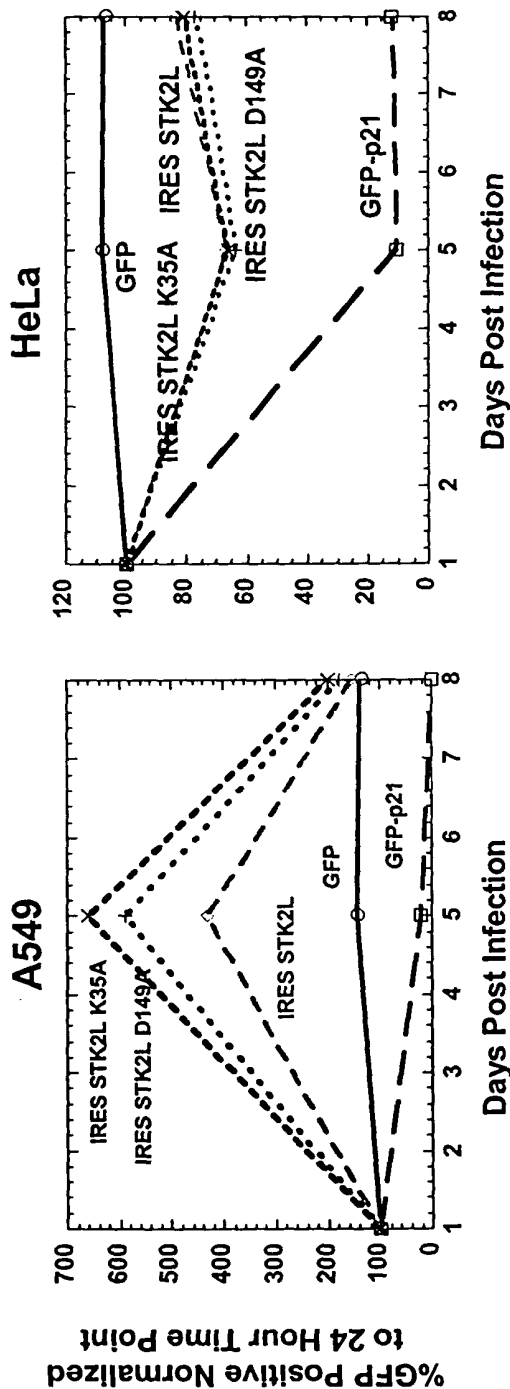


FIGURE 37

%GFP Positive at 24 Hours		
	A549	HeLa
GFP	52.8	59.0
GFP-p21	11.0	23.1
IRES STK2L	0.80	0.64
IRES STK2L K35A	1.79	2.3
IRES STK2L D149A	1.93	4.4

# IRES Hbo1 E508Q is Antiproliferative in A549 Cells

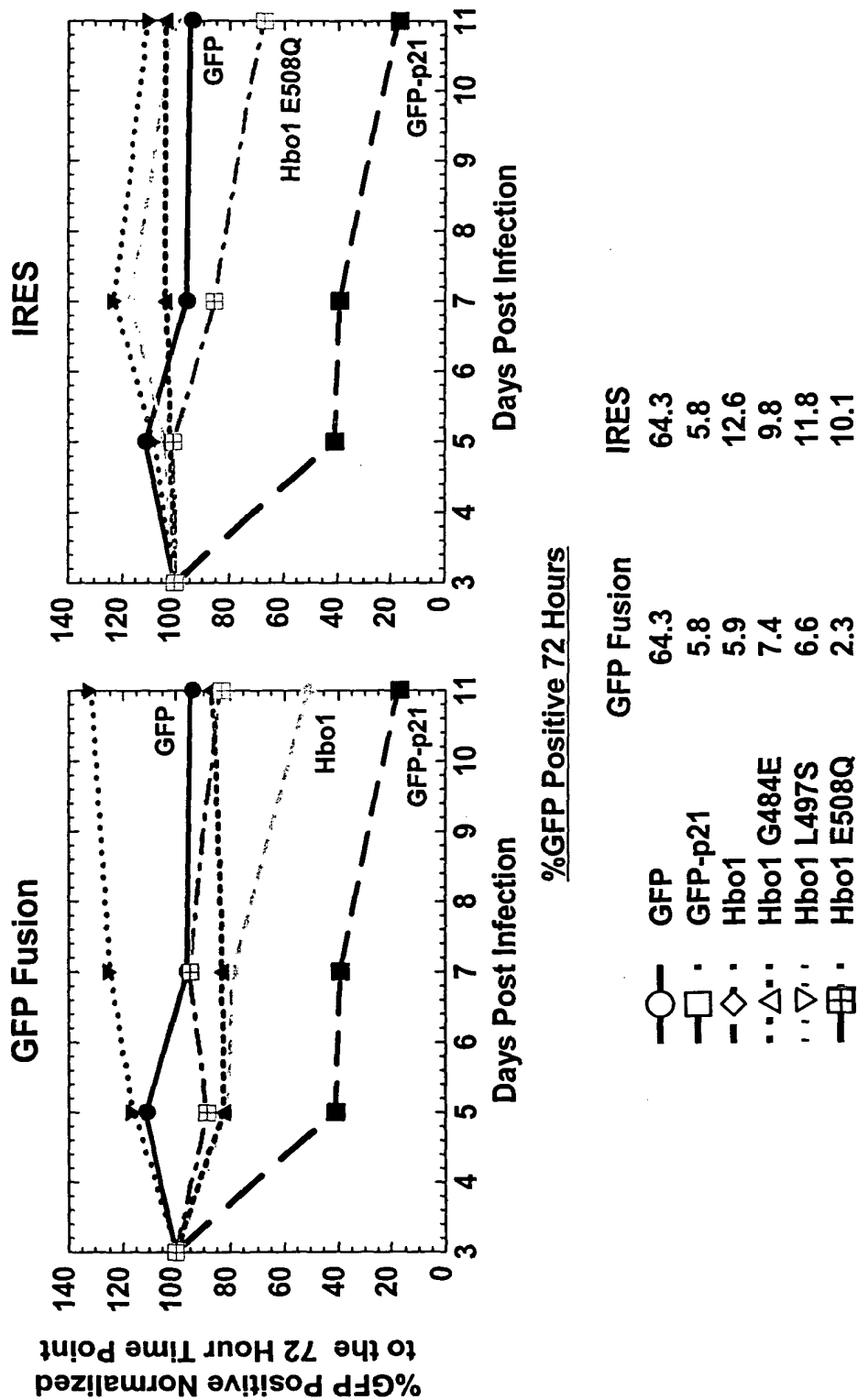


FIGURE 38

GFP-Hbo1 has a dominant negative effect which is not observed with the IRES construct



# No Significant Differences are Observed Between Hbo1 WT and Mutant Proteins in H1299 Cells

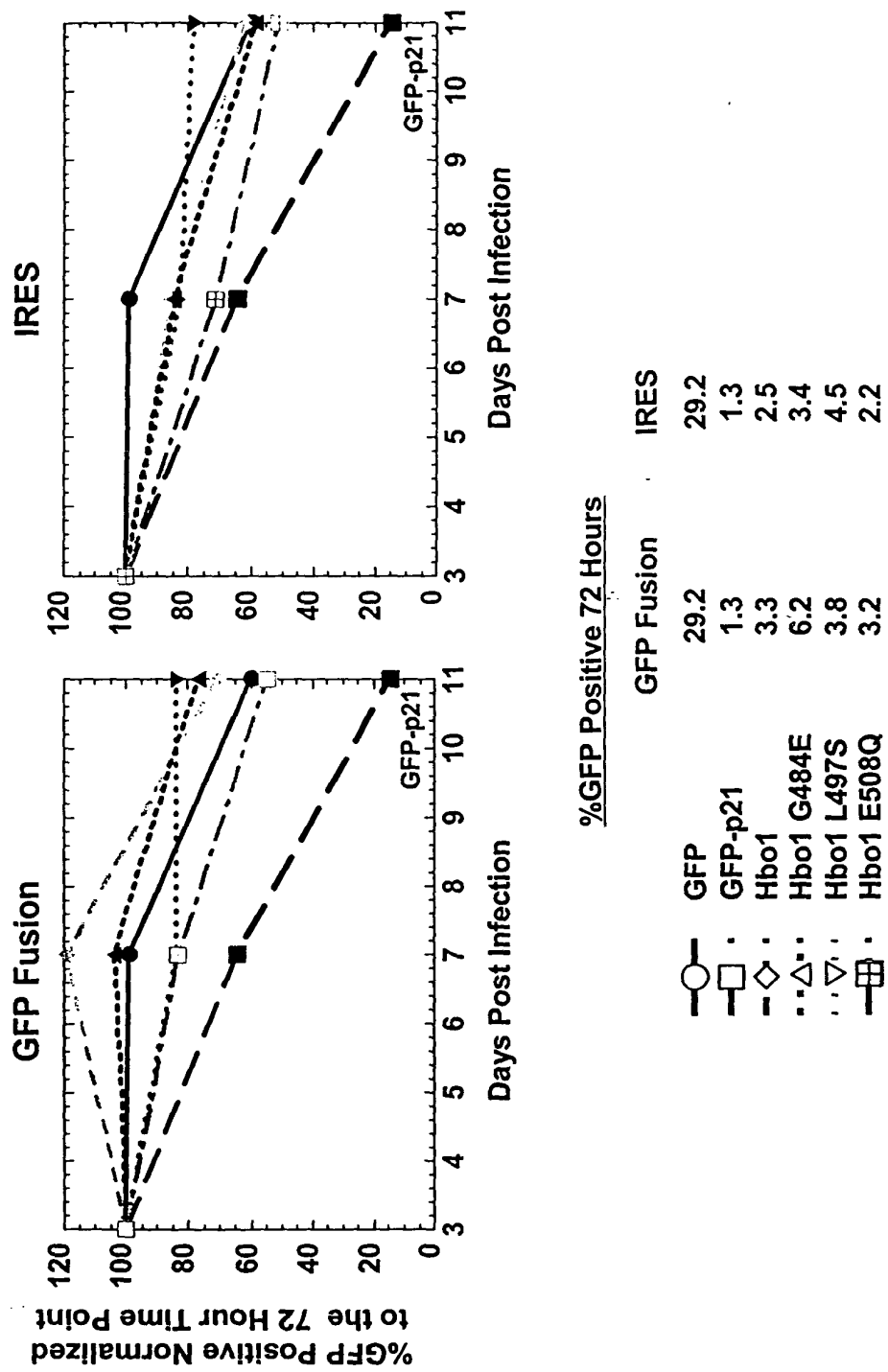
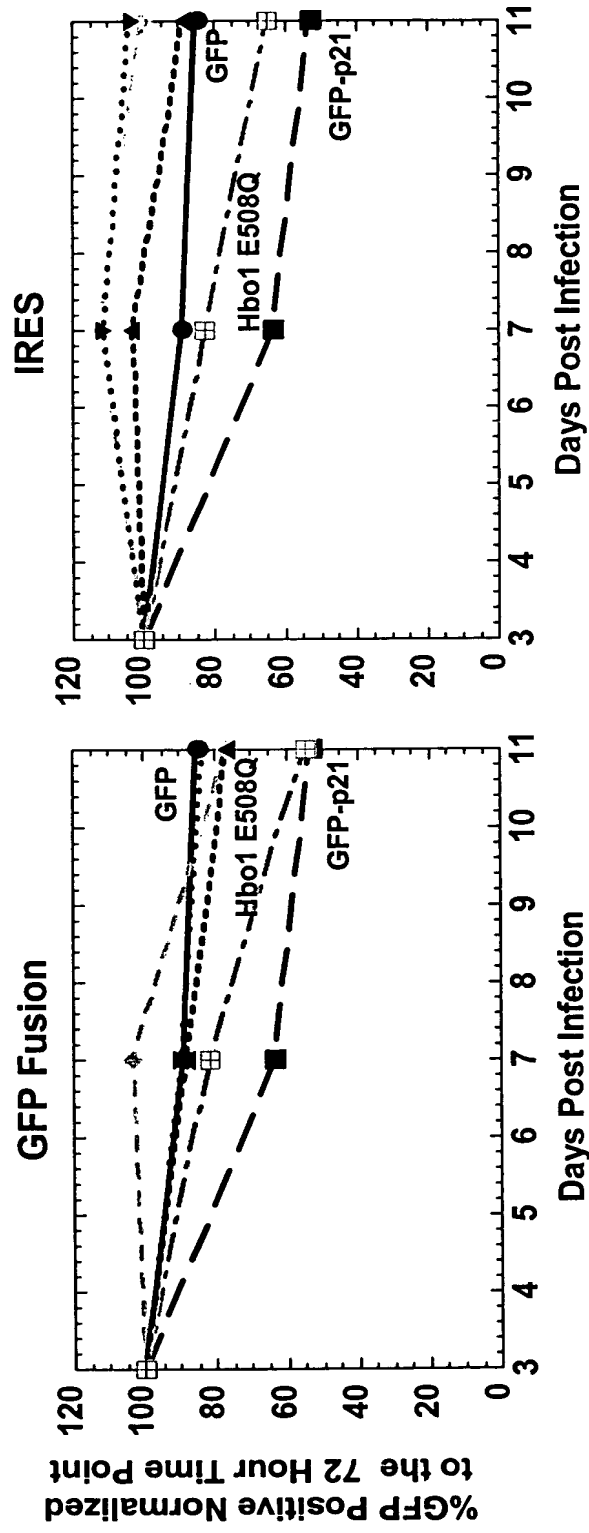


FIGURE 39

# Hbo1 E508Q is Antiproliferative in HeLa Cells



%GFP Positive 72 Hours

	GFP Fusion	IRES
GFP	100	100
GFP-p21	15.8	15.8
Hbo1	10.7	9.3
Hbo1 G484E	17.1	11.4
Hbo1 L497S	11.8	17.7
Hbo1 E508Q	10.2	5.2

FIGURE 40

Analyzing proliferation of Sorted Cells Expressing  
HRO1 WT or Dominant Negative Mutants

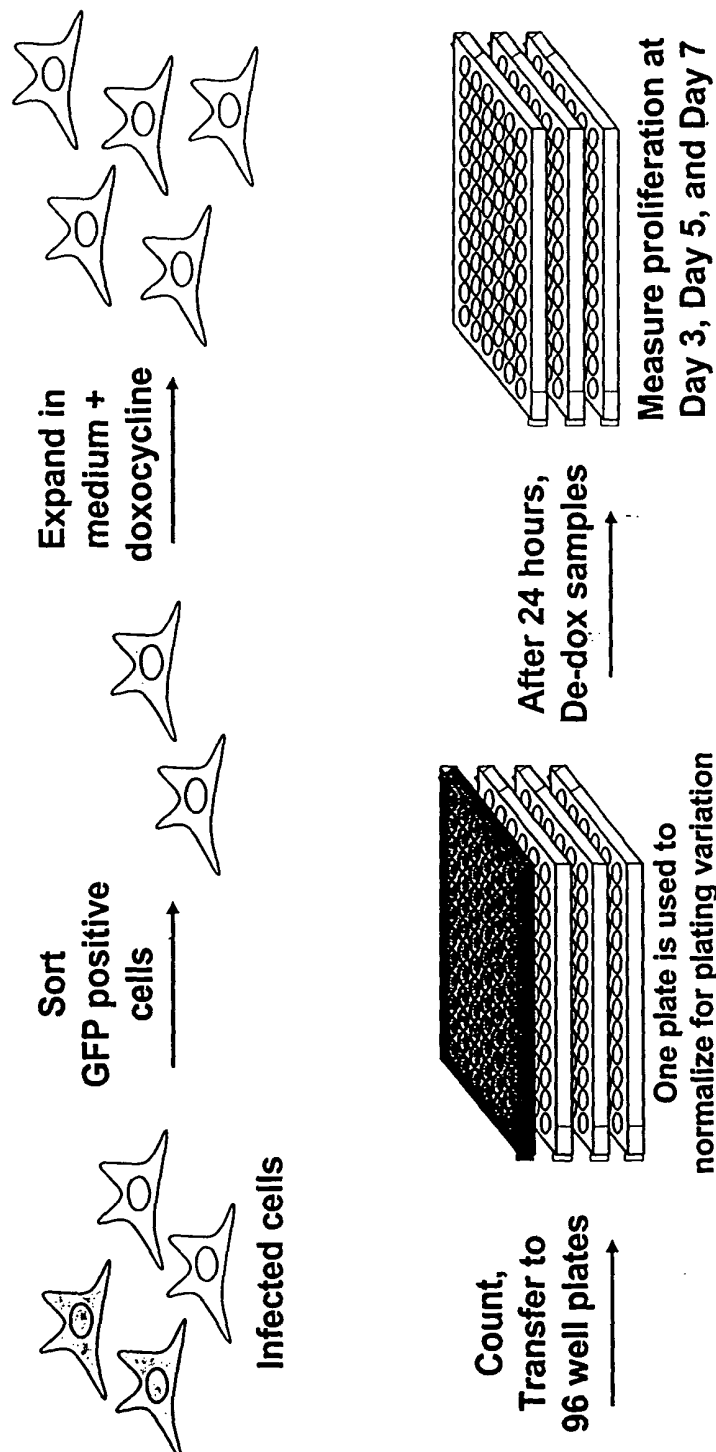


FIGURE 41

Proliferation is measured using the CyQuant Cell Proliferation Assay (Molecular Probes) which is based upon the fluorescence enhancement upon binding of a proprietary dye to cellular DNA

# HBO1 E508Q is Antiproliferative in A549 Cells

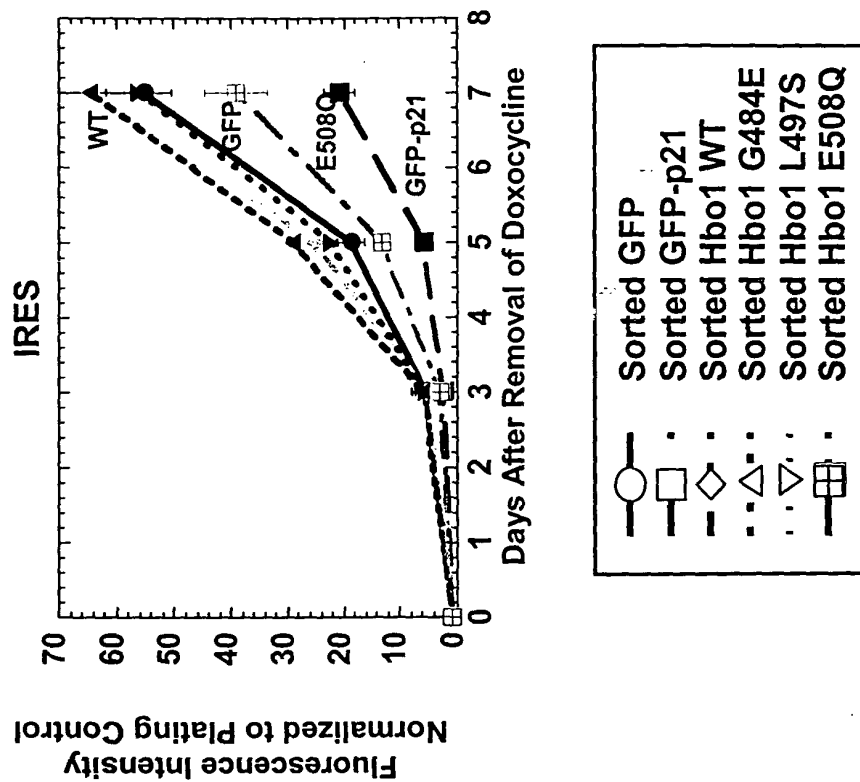


FIGURE 42

# HBO1 E508Q is Antiproliferative in HeLa Cells

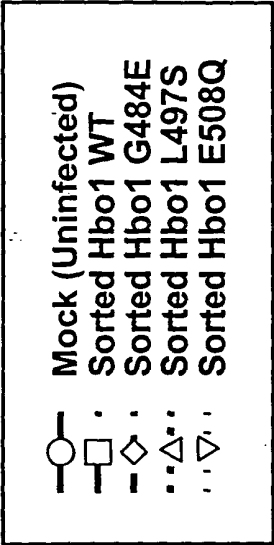
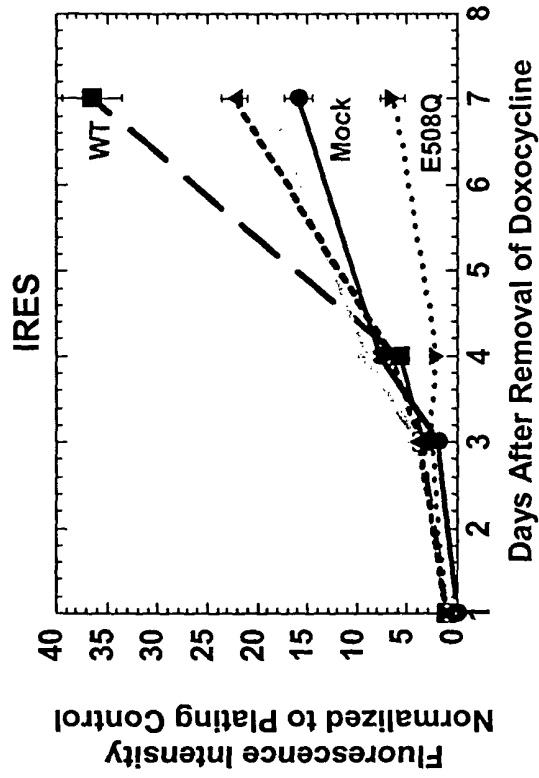


FIGURE 43

# HBO1-Specific siRNA Has an Antiproliferative Effect on A549 Cells

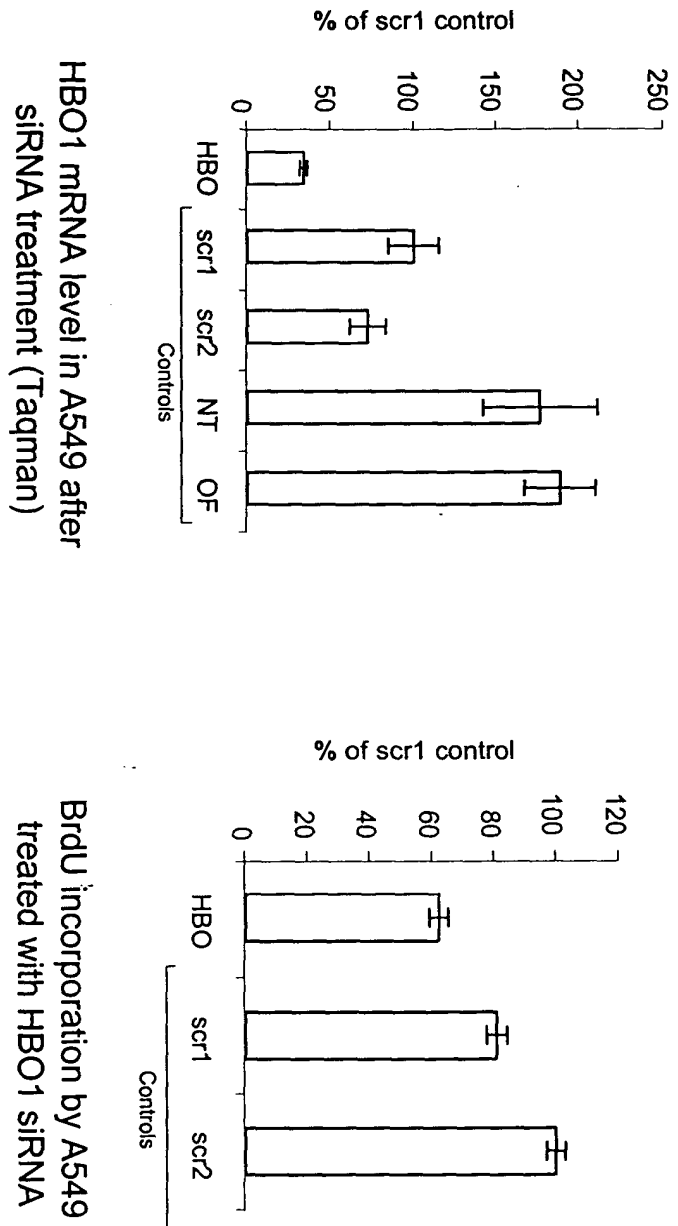


FIGURE 44

# HBO1-Specific siRNA Has an Antiproliferative Effect on H1299 Cells

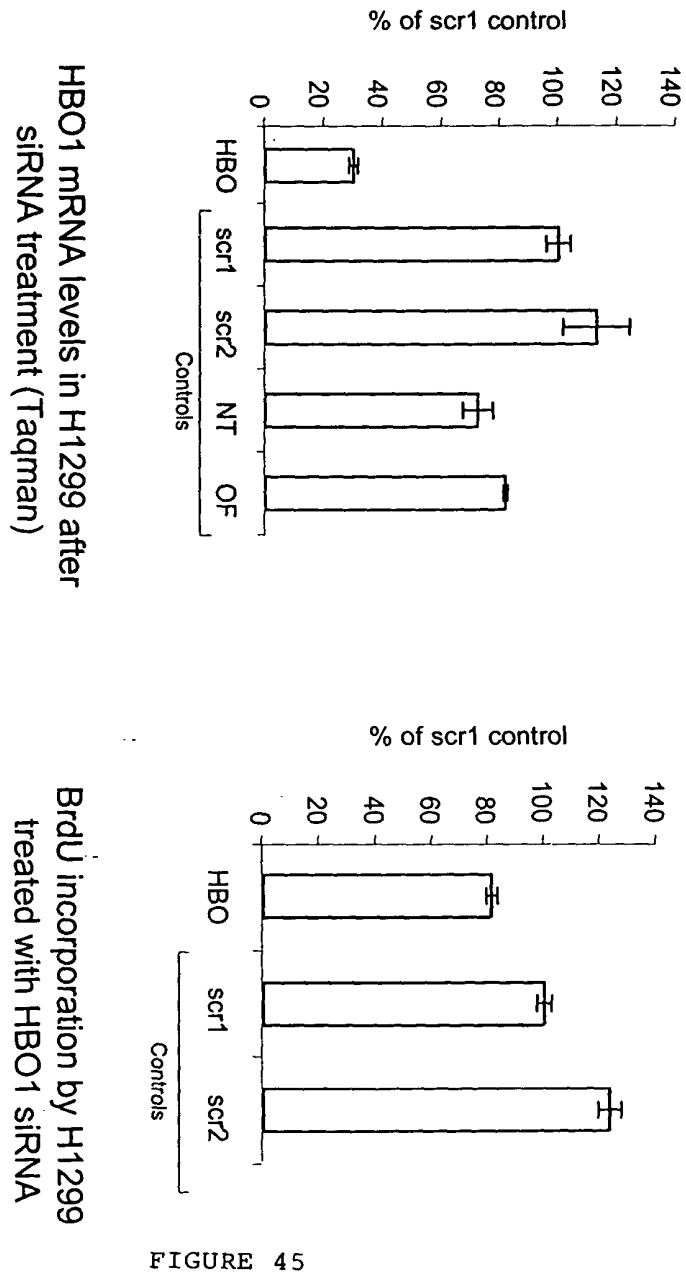


FIGURE 45

Taqman Analysis of PIM-1 Expression Using RNA  
from Tumor Cell Lines

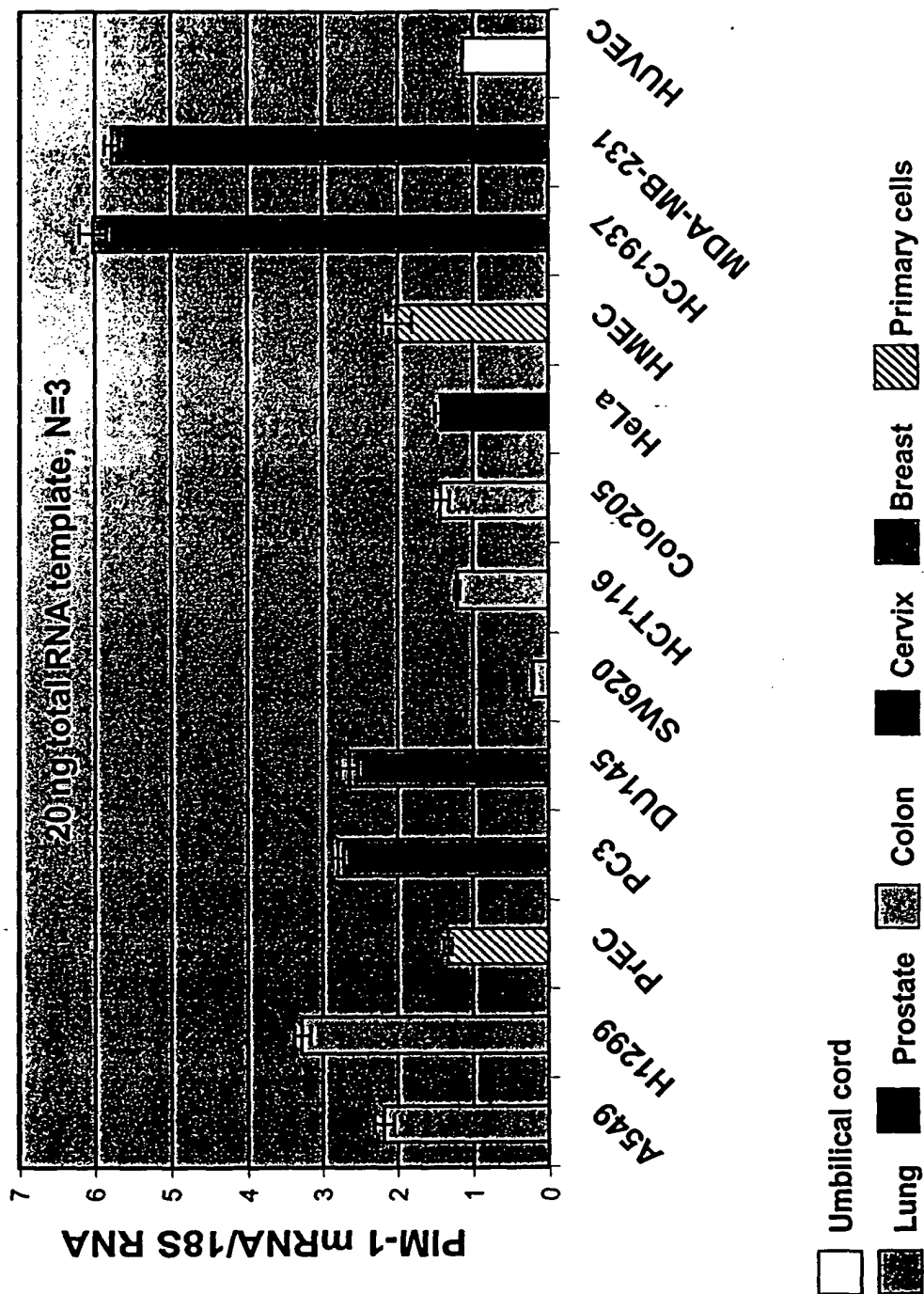


FIGURE 46



Taqman Analysis of PIM-1 mRNA Expression  
in Samples Obtained from Patients with Breast Carcinoma

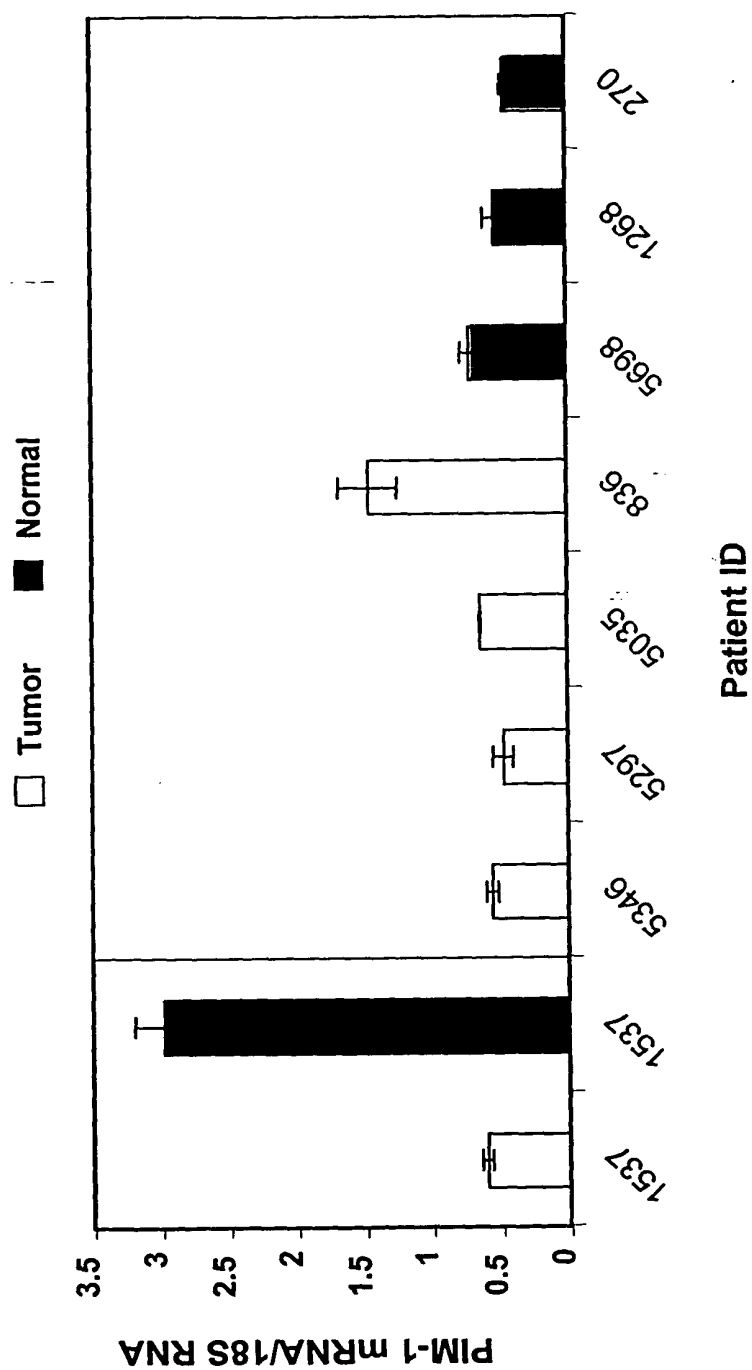


FIGURE 47

N = 3, 20 ng total RNA/sample

Taqman Analysis of PIM-1 mRNA Expression in Samples  
Obtained from Patients with Lung Carcinoma

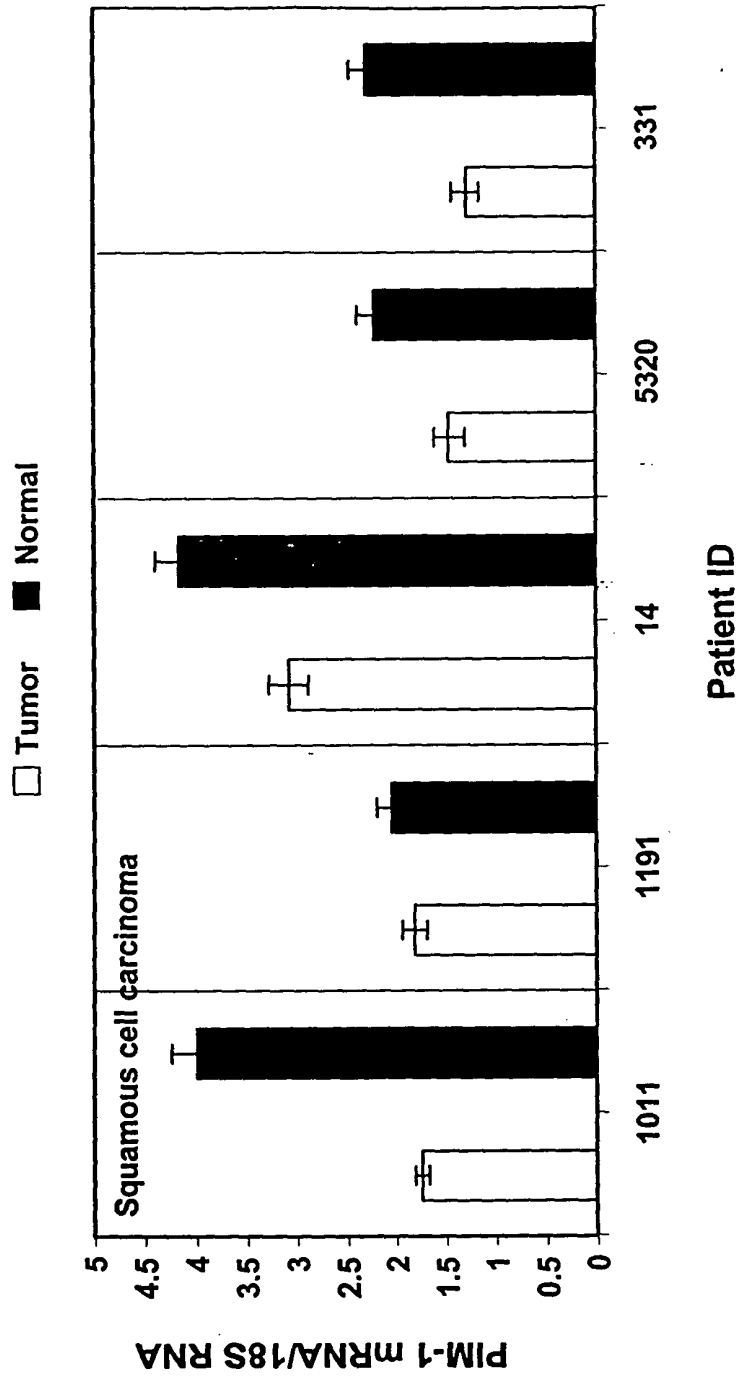


FIGURE 48

N = 3, 20 ng total RNA/sample

**%GFP Positive Normalized to the 72 Hour Time Point**

**GFP Fusion**

Days Post Infection	GFP	GFP-p21	Pim-1
3	100	100	100
4	100	100	100
5	100	100	100
6	100	100	100
7	100	100	100
8	100	100	100
9	100	100	100
10	100	100	100

**IRES**

Days Post Infection	GFP	GFP-p21	Pim-1
3	100	100	100
4	100	100	100
5	100	100	100
6	100	100	100
7	100	100	100
8	100	100	100
9	100	100	100
10	100	100	100

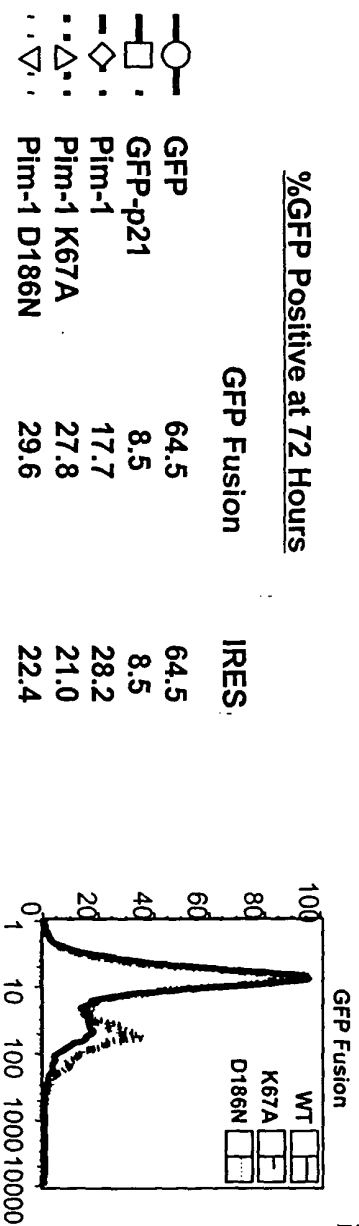
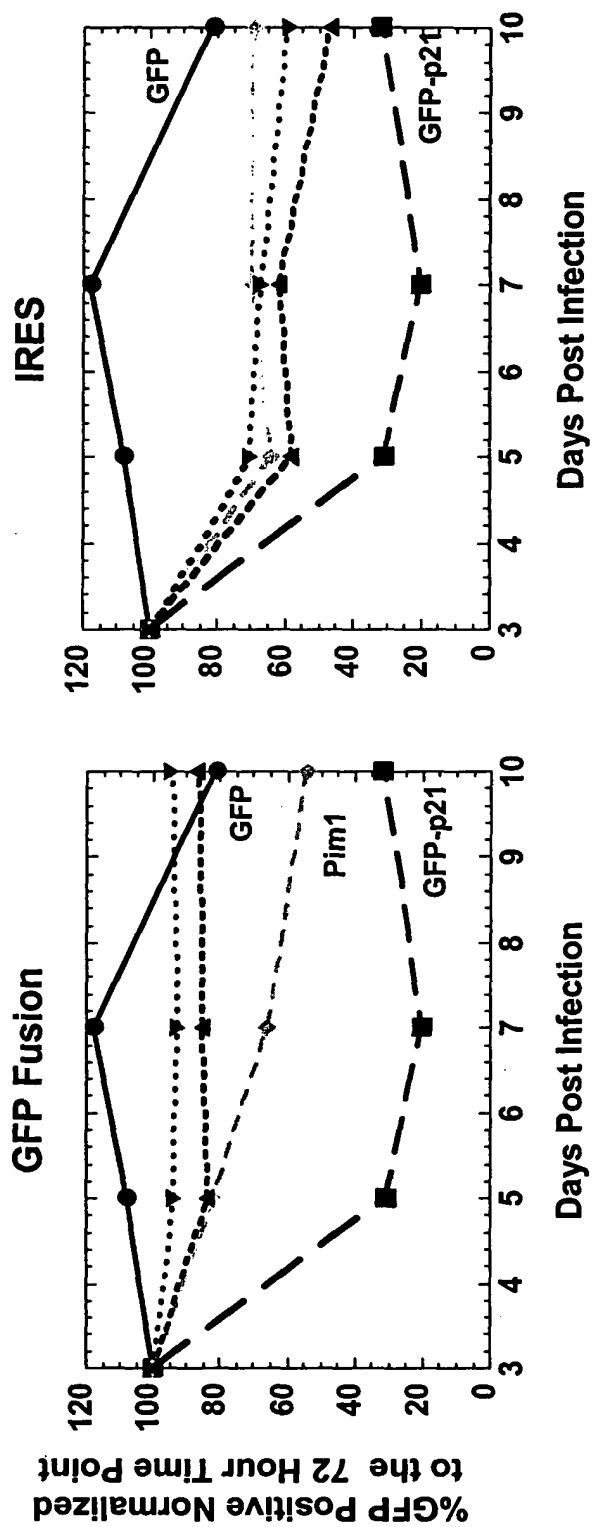


FIGURE 49

# In H1299 Cells, Expression of GFP-Pim-1 WT and all IRES constructs is Antiproliferative



%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	7.5	7.5
GFP-p21	0.44	0.44
Pim-1	3.6	0.92
Pim-1 K67A	2.8	0.81
Pim-1 D186N	2.6	1.1

FIGURE 50

# **PIM-1-Specific siRNA Has an Antiproliferative Effect on A549 Cells**

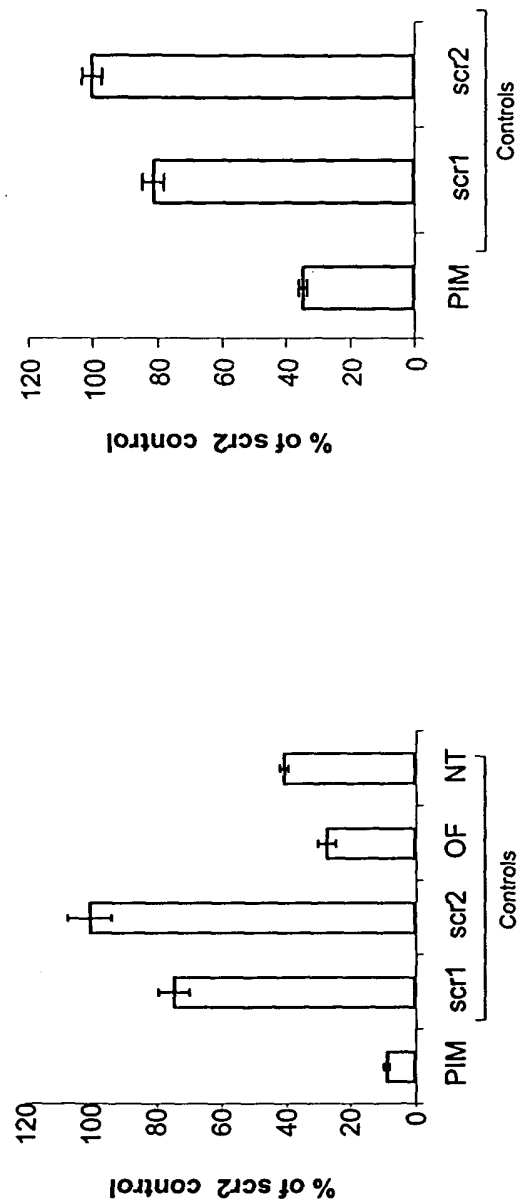


FIGURE 51

PIM-1 mRNA level in A549 after siRNA treatment (Taqman)

BrdU incorporation by A549 treated with PIM-1 siRNA

OF: oligofectamine, NT: no transfection

# **PIM-1-Specific siRNA Has an Antiproliferative Effect on HeLa Cells**

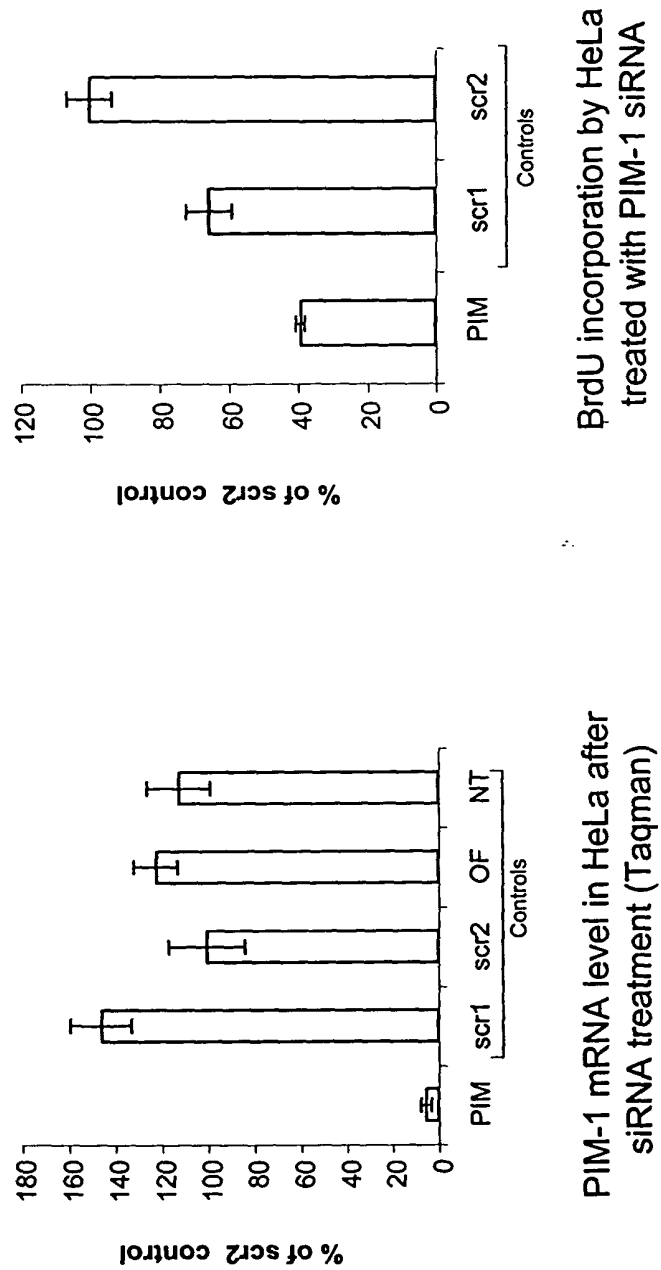


FIGURE 52

OF: oligofectamine, NT: no transfection

# **PIM-1-Specific siRNA Has an Antiproliferative Effect on H1299 Cells**

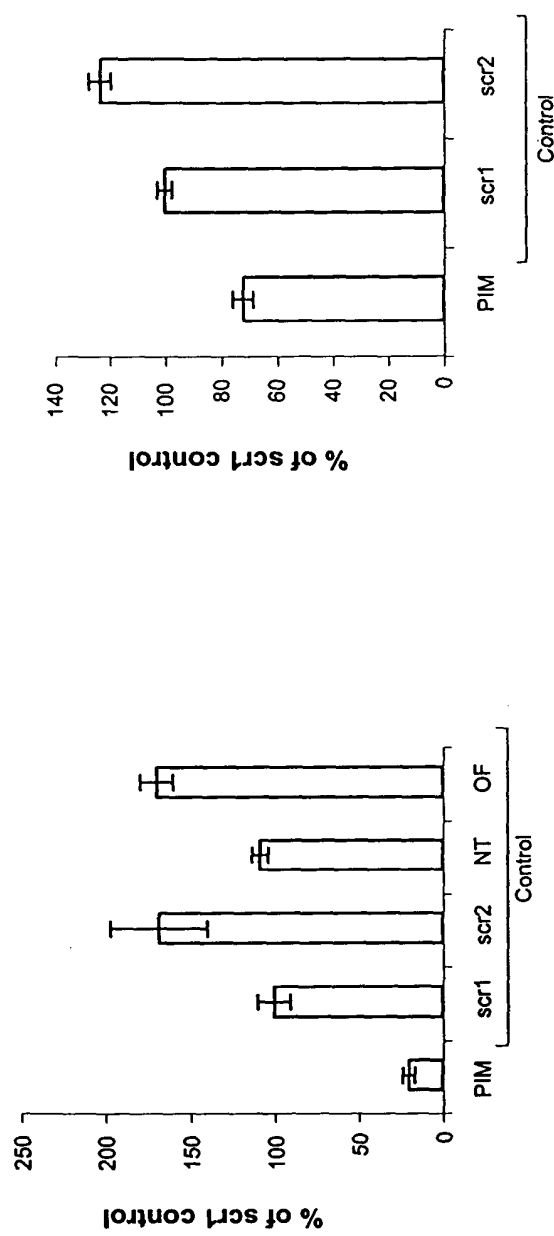


FIGURE 53

OF: oligofectamine, NT: no transfection

# **PIM-1-Specific siRNA Has an Antiproliferative Effect on HUVEC Cells**

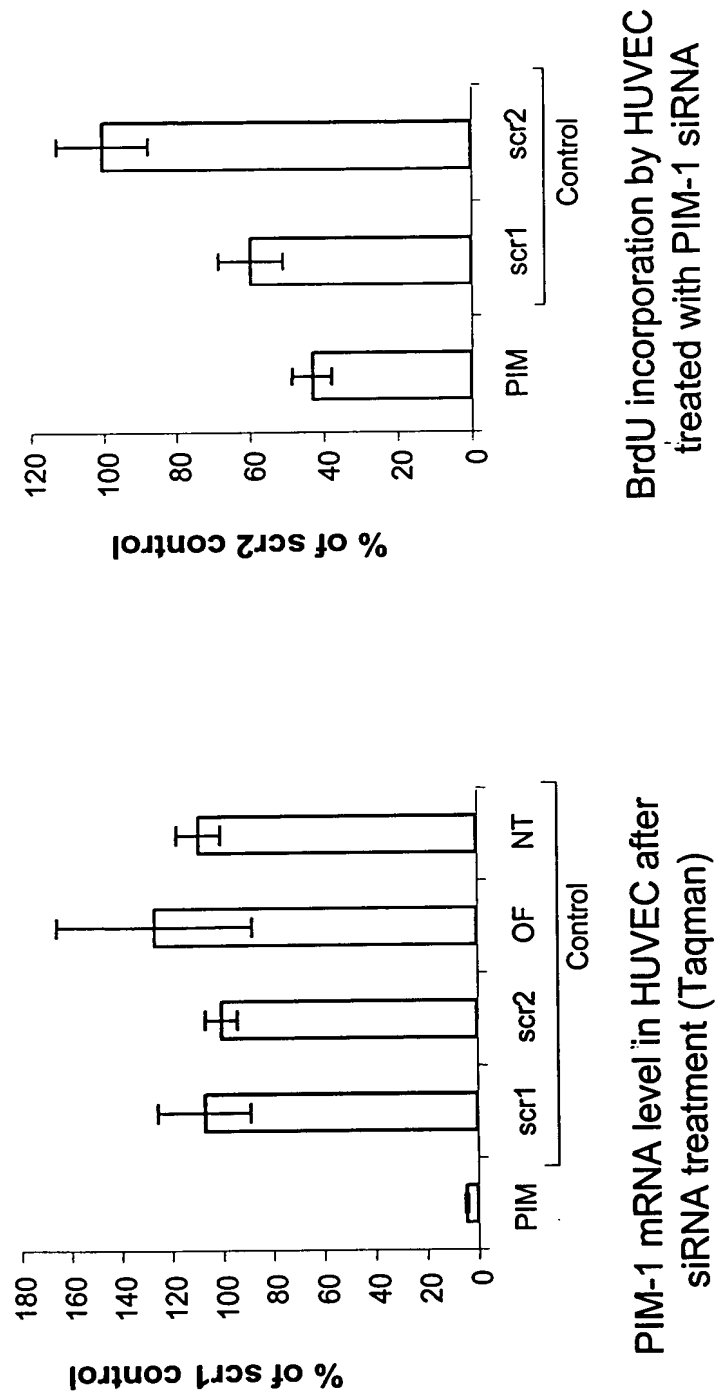
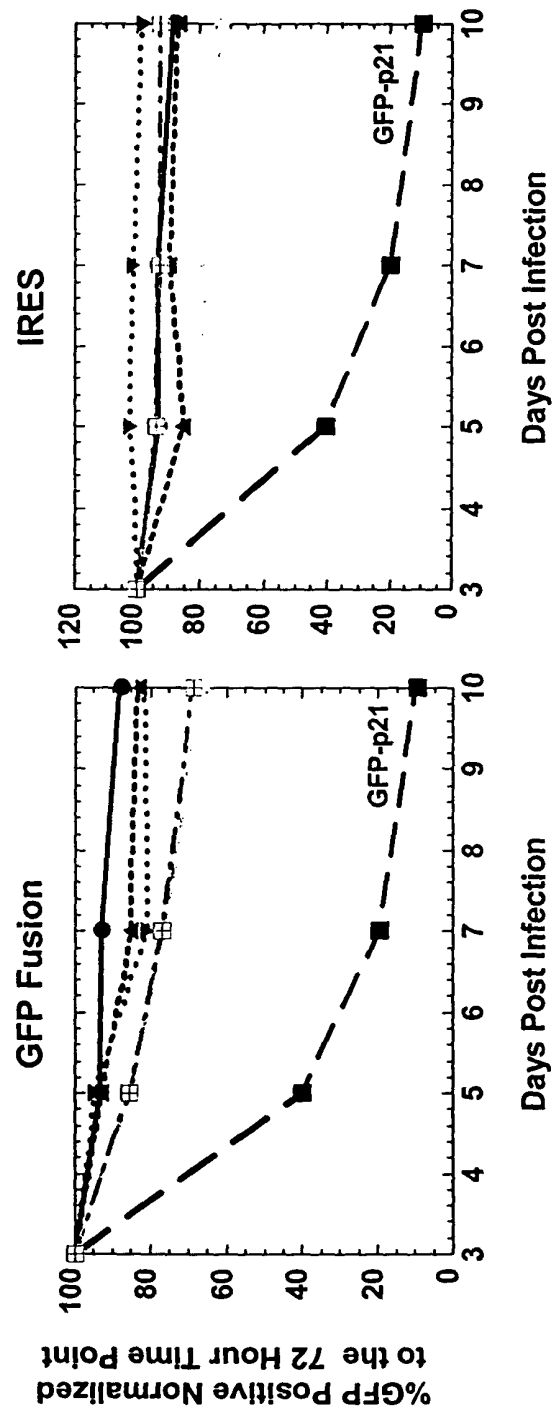


FIGURE 54

OF: oligofectamine, NT: no transfection



# No Antiproliferative Effects are Observed for Ape1 WT and Dominant Negative Mutants in A549 Cells

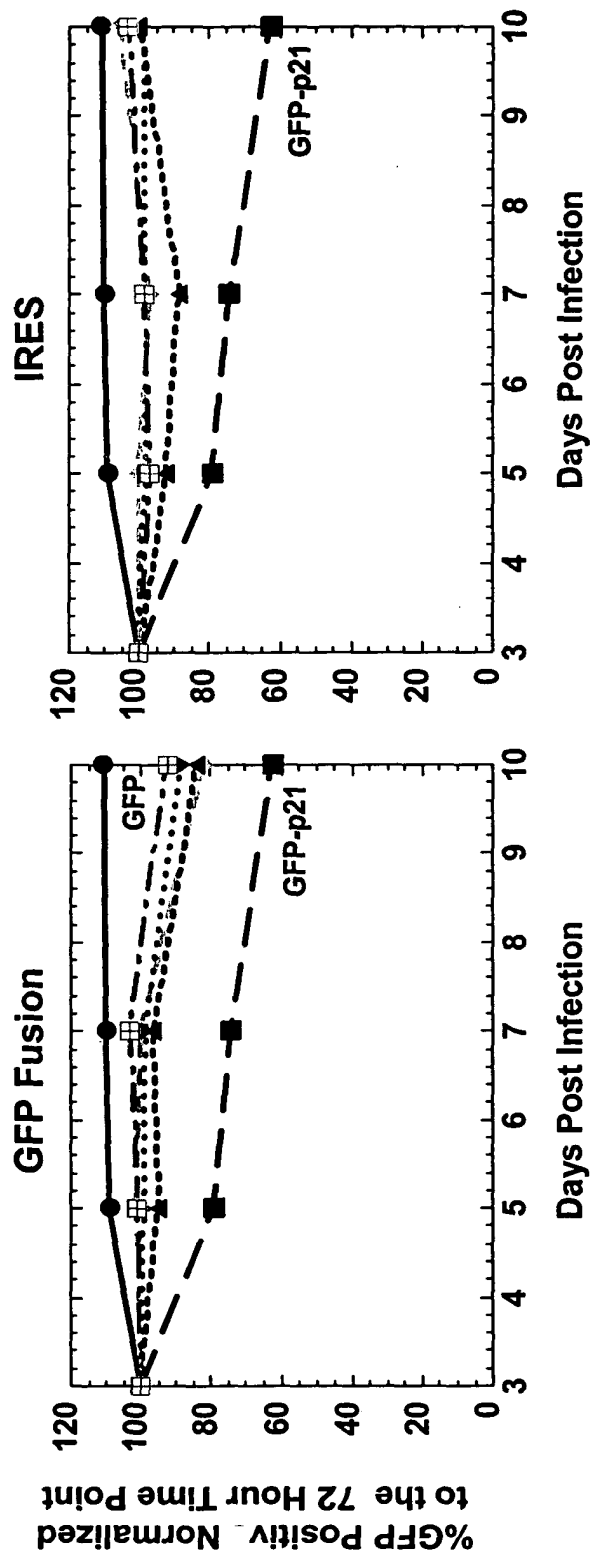


%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	66.4	66.4
GFP-p21	13.2	13.2
Ape1	13.2	13.6
Ape1 E96A	12.9	16.7
Ape1 D210A	14.3	11.3
Ape1 C65A	14.6	17.2

FIGURE 55

# GFP-Ape1 WT and Dominant Negative Mutants Have No Effect in H1299 Cells

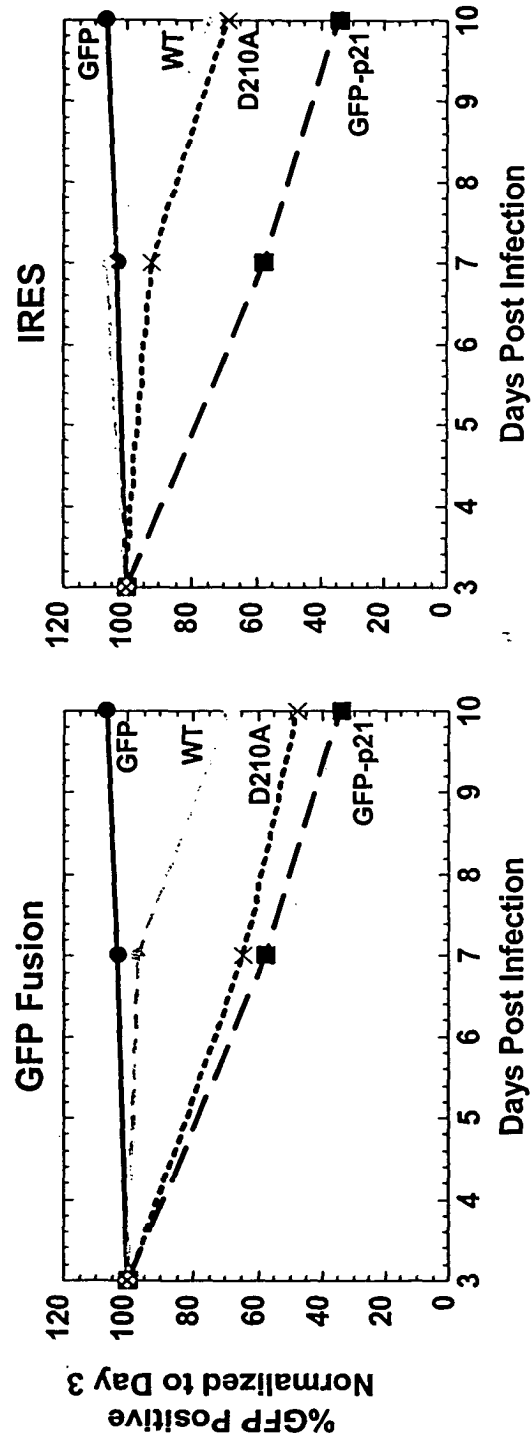


%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	49	49
GFP-p21	6.3	6.3
Ape1	8.2	7.1
Ape1 E96A	9.3	7.3
Ape1 D210A	8.4	4.9
Ape1 C65A	13.7	8.4

FIGURE 56

# Both Ape1 WT and Ape1 D210A Are Antiproliferative in HMEC Cells

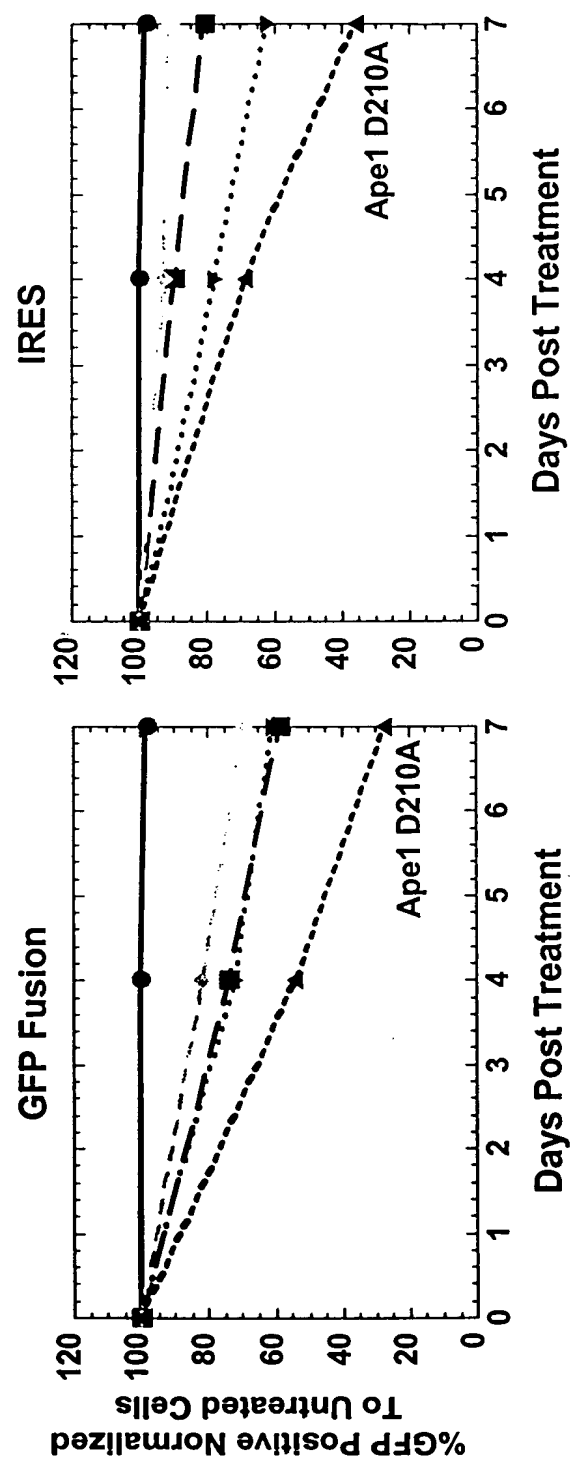


%GFP Positive (Day 3)

	GFP	IRES
GFP	30.7	30.7
GFP-p21	5.6	5.6
Ape1 WT	3.6	4.8
Ape1 D210A	5.2	4.2

FIGURE 57

# Ape1 D210A Sensitizes A549 Cells to Methyl Methanesulfonate Treatment



At 72 hours after infection, A549 cells were treated with 3mM MMS for 60 min.

%GFP Positive at Day 3		
	GFP Fusion	IRES
○ — GFP	64.8	64.8
□ — Ape1	15.7	6.2
◇ — Ape1 E96A	17.2	9.9
△ — Ape1 D210A	11.3	6.1
▽ — Ape1 C65A	16.8	3.3

FIGURE 58

# Ape1 WT and C65A Are Protective in A549 Cells Treated with Bleomycin

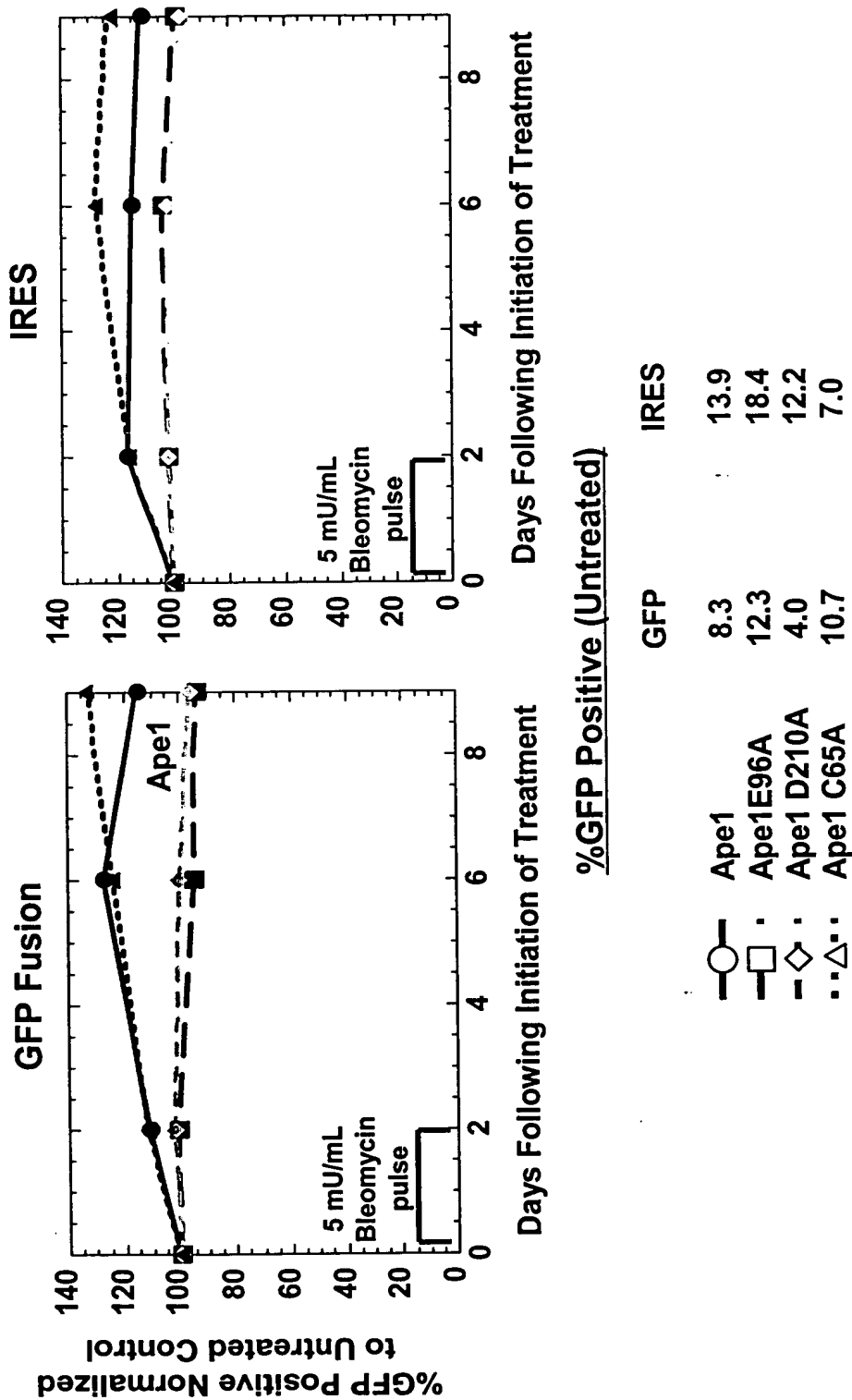


FIGURE 59

These results are consistent with those published by Robertson et al., *Cancer Res.* 2001 showing that overexpression of Ape1 in the tumor line NT2 confers resistance to bleomycin treatment.

# Ape1 WT and C65A Are Protective in HeLa and H1299 Cells Treated with Bleomycin

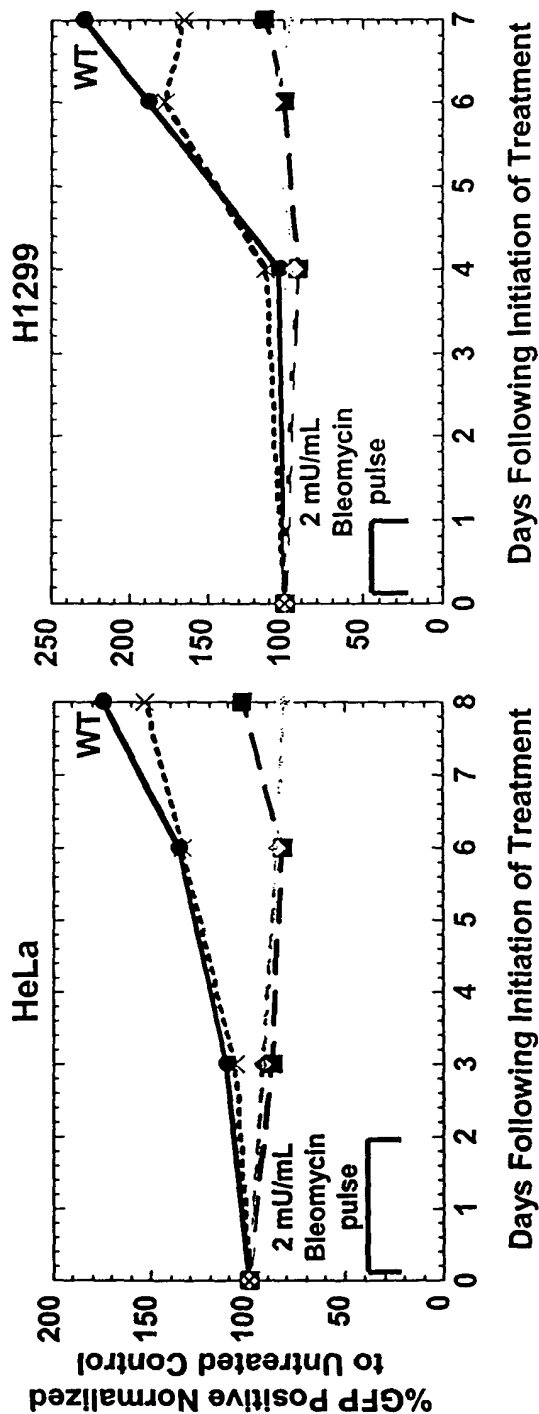


FIGURE 60

## %GFP Positive (Untreated)

	HeLa	H1299
Ape1 WT	11.4	2.8
Ape1 E96A	12.4	5.2
Ape1 D210A	36.3	3.6
Ape1 C65A	36.1	3.6

IRES-Ape1 constructs were used for these experiments.

Tagman Analysis of CK2a Expression  
Using RNA from Tumor Cell Lines

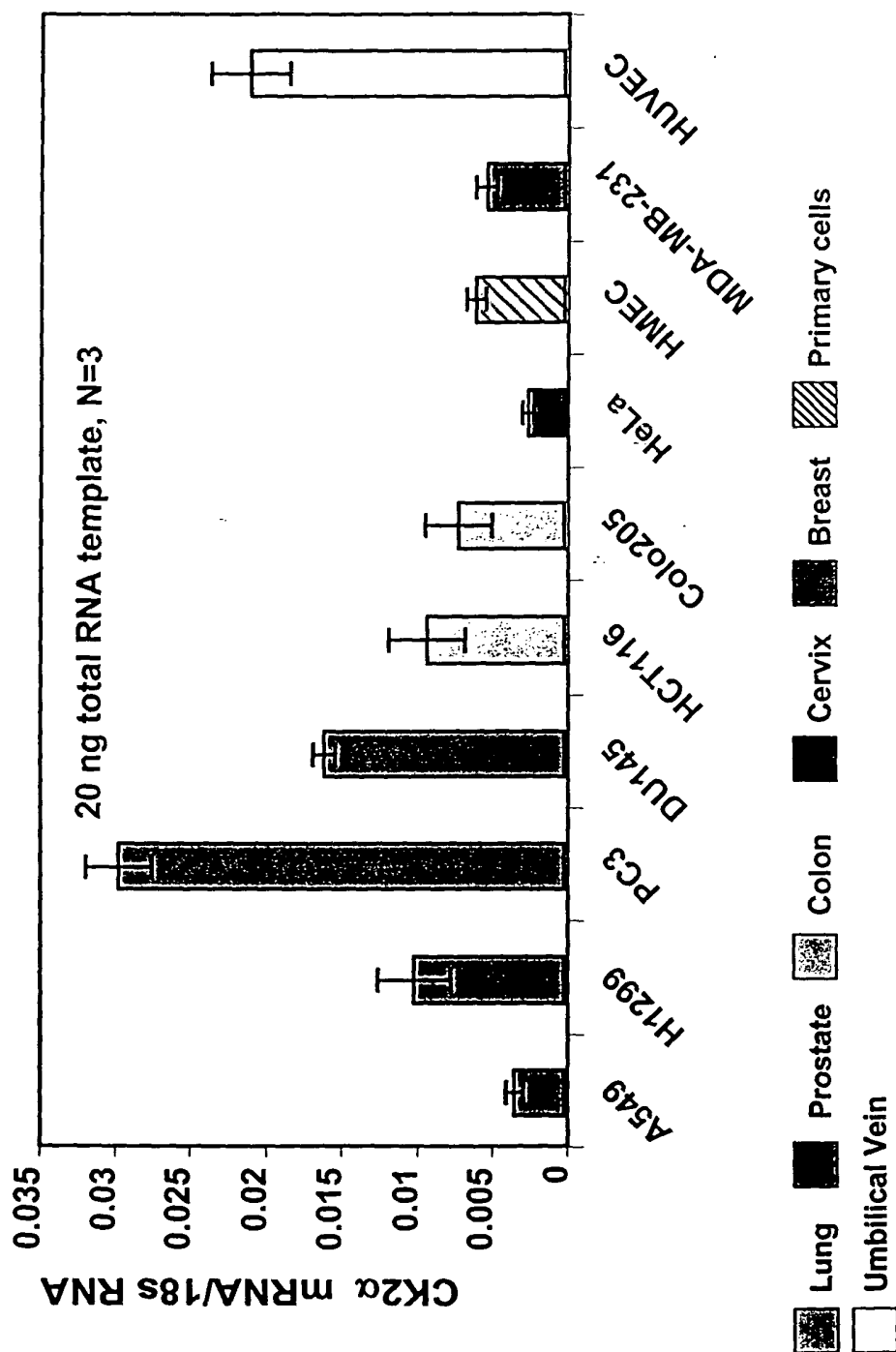


FIGURE 61

# Dominant Negative Mutants for CK2α

**Point mutants : K68A,D175N- K68A** corresponds to a mutation considered essential for the phototransfer reaction in the kinase domain (Oncogene. 2001 Apr 12;20(16):2010-22. PMID: 11360185 ), D175N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

```

*->yelleklGeGsfGkVykakhkdkgtgiVavKilkkkesikekrflr
Y+l++klG+G +++V++a+++ ++++V+vKilk ++k+ + r
CK2alpha 39 YQLVRKLGRGKYSEVFEAINI-TNNEKVVVKILK--PVKKKK--IKR 80

EiqilkrLs.HpNIvrligvfed.tddhlylvmEymegGdLfdyllrrngg
Ei+il +L++ pNI++l +++ d+ ++ + lv+E+++++d +++ + +
CK2alpha 81 EIKILENLRGPNITLADIVKDPVSRTPALVFEHVNTDFKQLYQTLT- 129

plsekeakkialQilrGleYlHsngivHRDLKpeNILLdendgtvKiaDF
+ ++++++il++l+Y+Hs+gi+HRD+Kp N+++++++ +++++D+
CK2alpha 130 ---DYDIRFYMYEILKALDYCHSMGIMHRDVKPHNVIMIDHEHRKRLIDW 176

GLArlllesssklttfvGTpwYmmAPEvileg.rgysskvDVWSlGvilyE
GLA ++++++ ++ +v ++++ PE+ l + ++Y+ D+WSlG++L+
CK2alpha 177 GLAEFYHPGQYNNVRVASRYFK-GPEL-LVDYQMYDYSLDMWSLGCMLAS 224

lltggplfpgadlpafg.gd.evdqli.if.vlklpfsdelpktridpl
+ ++++++f+ ++++++ ++++++ ++ +++++ +d++++k++i+
CK2alpha 225 MIFRKEPFF-----HghDnYDQLVRIAKVLGTEDLYDYIDKYNIELD 266

eelfriiikrp.....glrlplpsncSeelkdLlkkcLnkDPskRpGsa
+ +i+ r+++++ +++ ++++++++S++++d+l+k+L+++D ++R+
CK2alpha 267 PRFNDILGRHsrkrwerFVHSENQHLVSPEALDFLDKLLRYDQSRLL--- 313

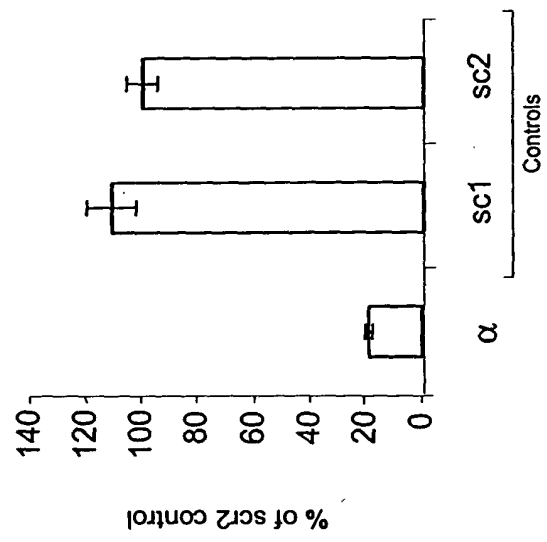
takeilnhpwf<-*
ta+e++++hp+f
CK2alpha 314 TAREAMEHPYF 324 Bold= the catalytic residues

```

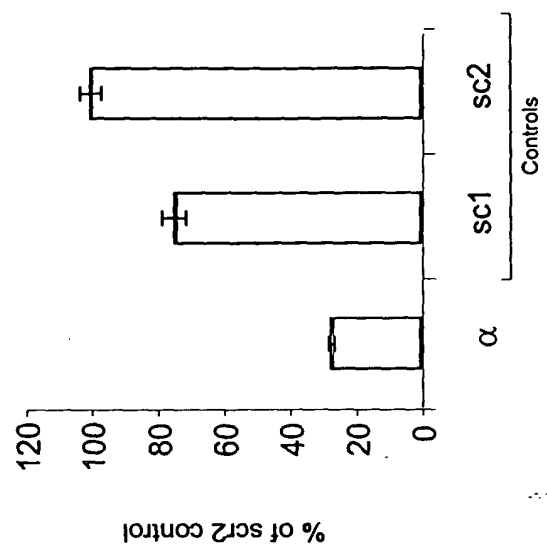
FIGURE 62



# **CK2 $\alpha$ -Specific siRNA is Antiproliferative in H1299 Cells**



**CK2 $\alpha$  mRNA level in H1299 after siRNA treatment (Taqman)**



**BrdU incorporation by H1299 treated with CK2 $\alpha$  siRNA**

**FIGURE 63**

Sc1 and sc2 refer to scrambled siRNA controls

Taqman Analysis of KNIAMRE Expression  
Using RNA from Tumor Cell Lines

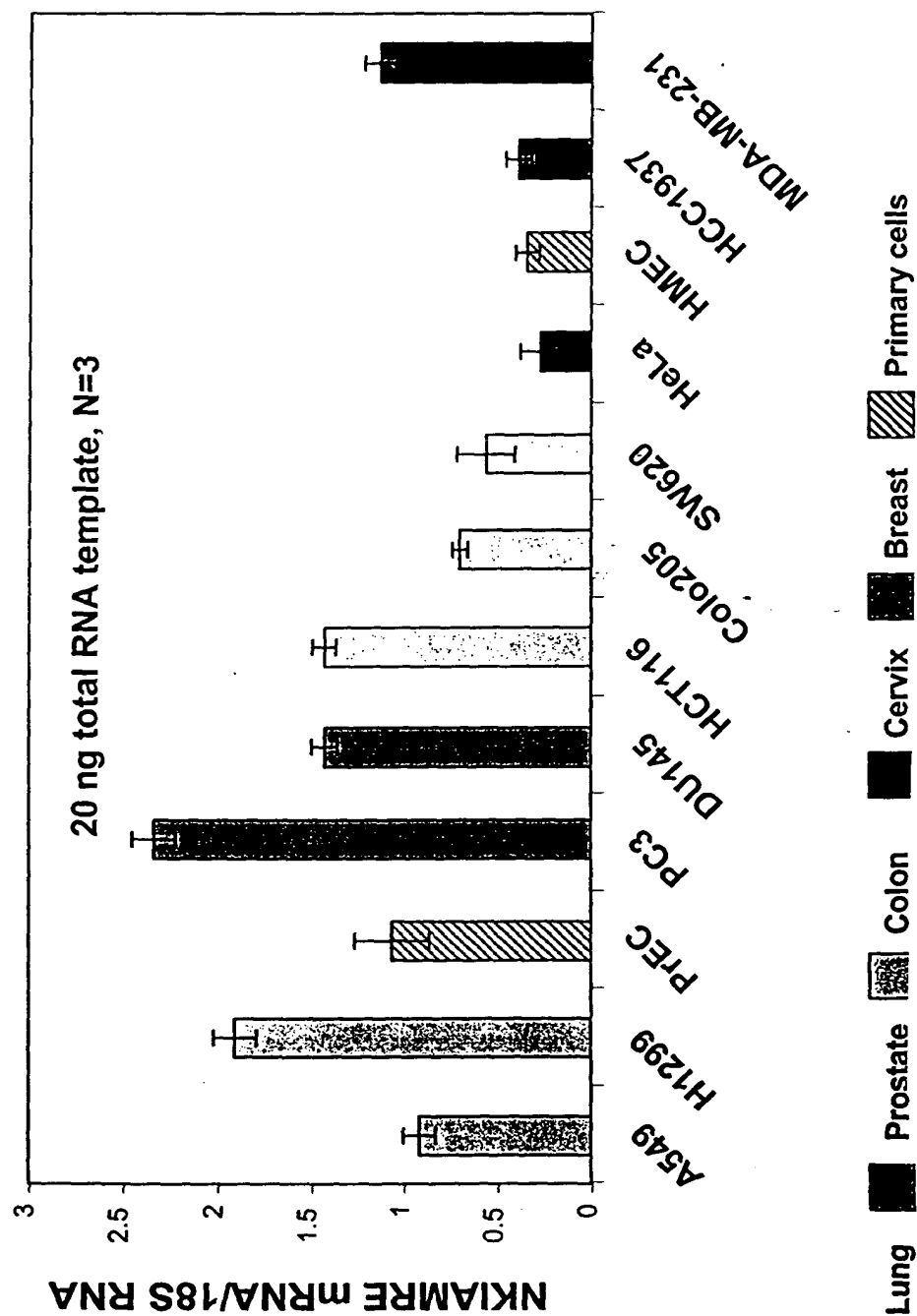


FIGURE 64

# Dominant Negative Mutants for NKIAMRE

## NKIAMRE active site mutants K33A, D143A

CDK2	MENFQKVEKIGEGTYGVVYKARNKLTGEVVVALKKIRLDTETEGVPSTAIRESLLKELNH	○
NKIAMRE	MEMYETLGKVGEGSYGTMKCKHKNTGQIVAIKIFYPEREQS-VNKIAMREIKFLKQFHH	
	** : : : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
CDK2	PNIVKLLDVIHTENKLYLVFEFLHQDLKKFMDASALTGIPLPLIKSYLFQLLQGLAFCHS	
NKIAMRE	ENLVNLIIEVFRQKKIHLVFEFIDHTVLDELQHYCHG-LESKRRLRKYLFQILRAIDYLS	
	* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
CDK2	HRVLRDLKPQNLLINTEGAIKLADFGLARAFGVPRVRYTHEVVTWYRAPEILLGCKYY	○
NKIAMRE	NNIIHRDIKPENILVSQSGITKLCDFGFARTLAAPGDIYDYVATRWYRAPELVLKDTSY	
	: : : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
CDK2	STAVDIWSLGCIFAEMVTRRALFPGDSEIDQLFRITLGTPTDEVVWPGVTSMPTYK-PS	
NKIAMRE	GKPVDI WALGCMIIEMATGNPYLPSSDDLHLHKIVLKVGNLSPHLQNI FSKSPIFAGVV	
	... * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
CDK2	FPKWAR-QDFSQVPPLEDEGRSLLSQMLHYDENKRI SAKAALAHFFQD--VTKPVPH	
NKIAMRE	LPQVQHPKNARKKYPKLNGLLADIVHACLIQIDPADRISSDDLHHEYFTRDGFIEKFMPE	
	: * : : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *	
CDK2	LRL-----	
NKIAMRE	LKAKLLQEAKVNSLIKPKESSKENELRKDERKTVYTNLTLLSSSVLGEIEKEKPKPEIKV	
	* :	
CDK2	-----	
NKIAMRE	RVIKVKGGRGDI SEPKKKEYEGLGQQDANENVHPMSPDTKLVTI EPPNPINPSTNCNGL	
	-----	
CDK2	-----	
NKIAMRE	KENPHCGGSVTMPPI NLITNSNLMAANLSSNLFPSPVR	○ Mutation site

FIGURE 65

# Dominant Negative Mutants for FEN1

FEN1 active site mutant D86A and D181A (PMID: 8621570, 10409728)

XPG_N domain*	-->MGIkGLlpiLkpvapeairsvsIEalegYYkvLAiDasiwLyqfLka	
FEN1	1	MGI+GL+++++vap+air++++i+++++g +++AiDas++++yqfL+a MGIQGLAKLIADVAPSAIRENDIKSYFG--RKVAIDASMSIYQFLIA 45
XPG_N domain		vRdqlgnnlenEeGettshlmglfSRlcrLldfgikPifVFDGgapndkK
FEN1	46	vR q g+ l+nEeGettshlmg+f+R+r+++++gIkP++VFDG++p +lK VR-QGGDVLQNEEGETTSHLMGMFYRTIRMENGIKPVYVFDGKPP-QLK 93
XPG_N domain		aetlqKRsarrqea<--*
FEN1	94	+++l+KRs+rr+ea SGELAKRSERRAEA 107
XPG_I domain*	-->rlmGIpyIvAPgVEAEAQcayLekkglvdgiiteDsDvLLFGaprll	
FEN1	146	+lmGIpy +AP+ EAEA ca+L+k+g+v+++++TeD+D+L FG+p+l+ SLMGIPYLDAPS-EAEASCAALVKAGKVAAATEDMDCLTFGSPVLM 191
XPG_I domain		rnLtlsgkksgPsitslkveieeidlesllrelgigklsregLidlailL
FEN1	192	r+Lt s++k k++i+e++l++++l+elgL ++eq++dl+iLl RHLTASEAK-----KLPIQEFHLSRILQELGL---NQEQFVLDLCILL 230
XPG_I domain		GcDYteG<--*
FEN1	231	G+DY+e+ GSDYCES 237
		○ Mutation site

FIGURE 66

# Expression of FEN1 Dominant Negative Mutants in A549 Cells is Antiproliferative

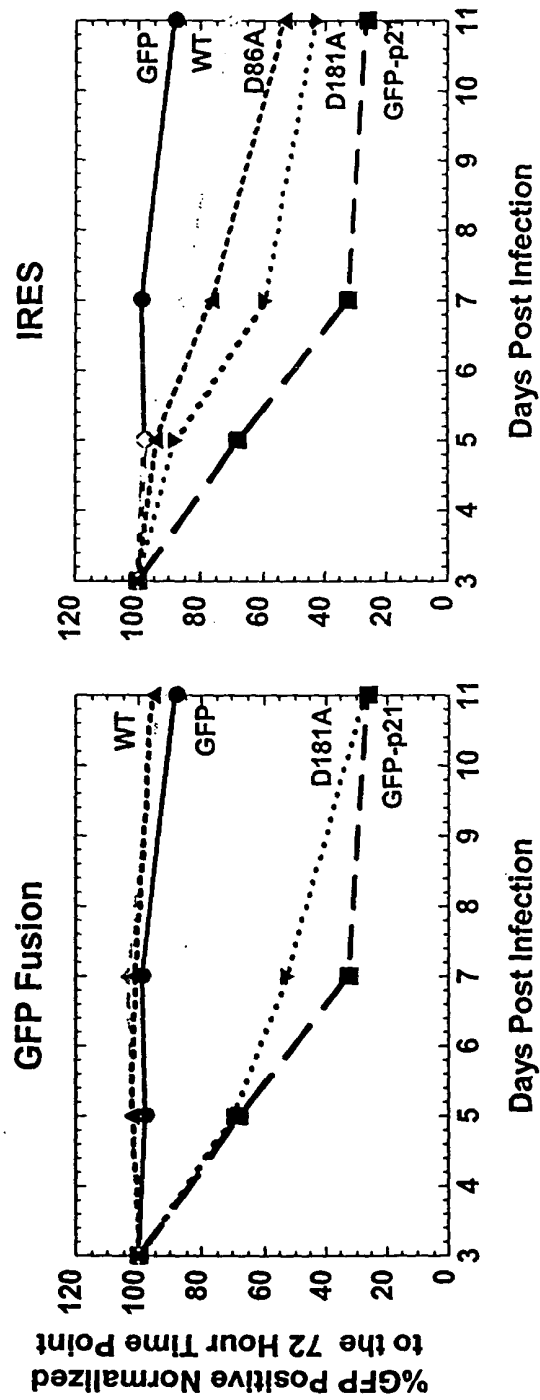


FIGURE 67

# Expression of FEN1 Dominant Negative Mutants is Antiproliferative in H1299 Cells

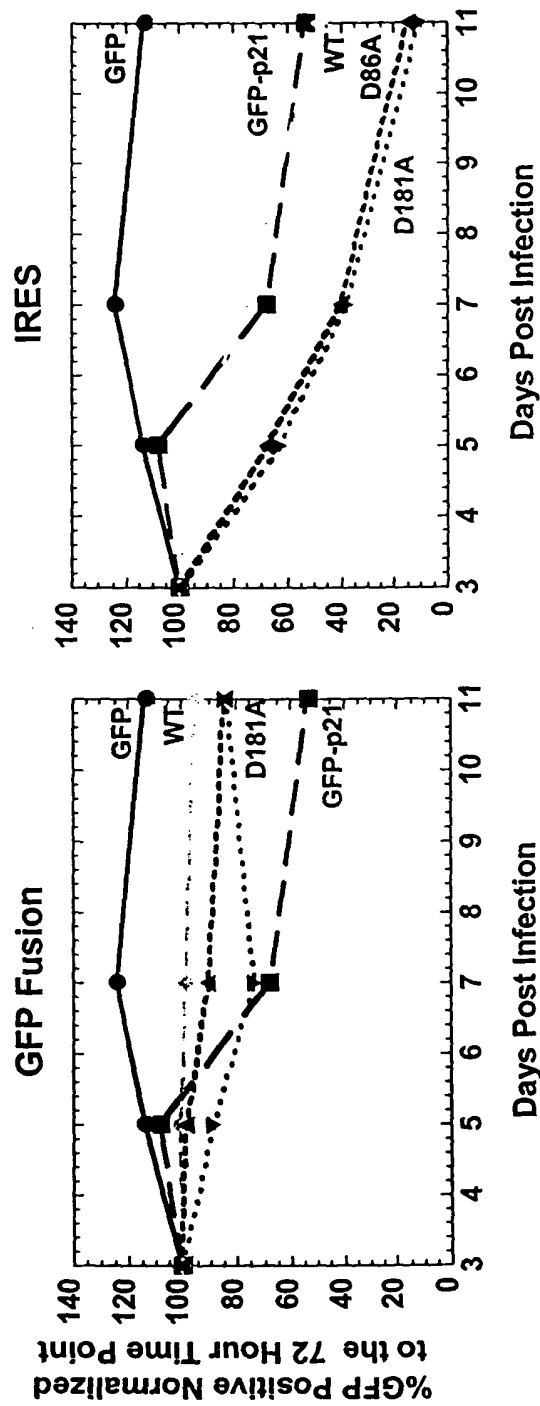


FIGURE 68

%GFP Positive at 72 Hours

	GFP Fusion	IRES
GFP	58.1	58.1
GFP-p21	3.9	3.9
Fen1 WT	34.4	25.9
Fen1 D86A	34.1	58.0
Fen1 D181A	48.3	59.7

### CDK3 active site mutants K33A, D145A

FIGURE 69

# Expression of CDK3 Dominant Negative Mutants Has No Antiproliferative Effect in A549 Cells

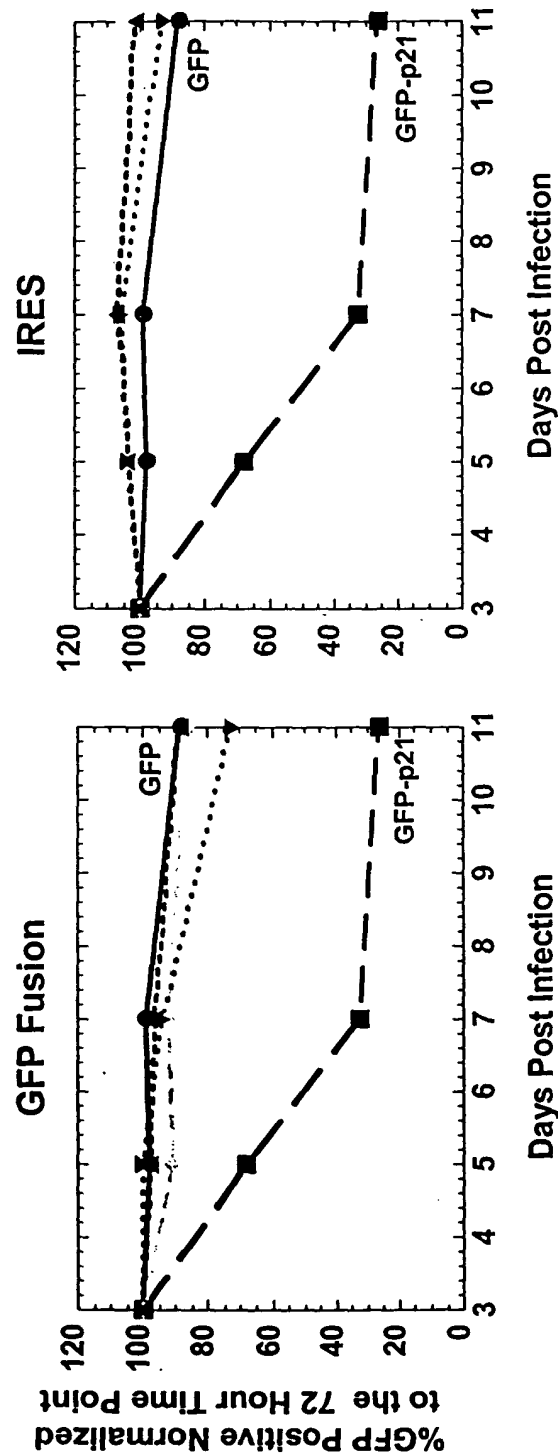


FIGURE 70

%GFP Positive at 72 Hours	
GFP Fusion	IRES
GFP	85.3
GFP-p21	19.5
CDK3 WT	57.2
CDK3 K33A	57.7
CDK3 D145A	51.5



# Expression of CDK3 Dominant Negative Negative Mutants Has No Antiproliferative Effect in H1299 Cells

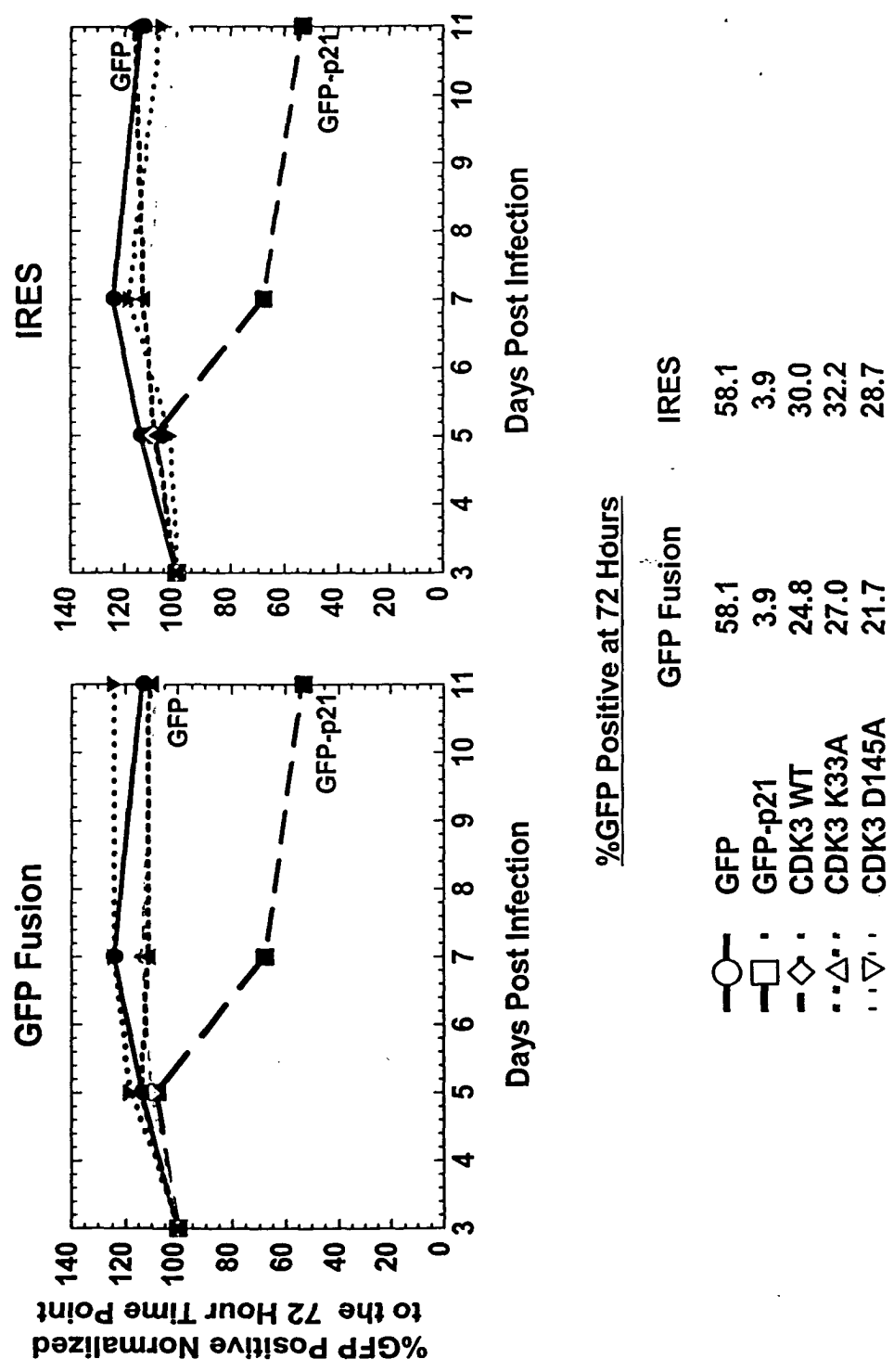


FIGURE 71

# Dominant Negative Mutants for HBO1

HBO1 active site mutants, G485E, L497S, E508Q, The G315 mutant, the L327S mutant and the E338Q mutant in yEsa1 abolished the catalytic activity (PNAS, p3561, 1998, MCB, p2515, 1999, Mol.Cell, p1195, 2000). G315 is involved in CoA binding (Mol.Cell, p1195, 2000).

HBO1 YHSPYPEYARLGRLYMCEFCCLKYMKSQTLRRHMAKCVWKHPGDEIYRKGSISVFEVD  
yEsa1 YFSPYPIELTDEDFIYIDDFTLQYFGSKKQYERYRKKCTLRHPPGNEIYRDDYVSFFEID  
\*.\*.\*.\*.\* : . :.\* : \* :.\* : \* :. :.\* : \* :. :.\* : \* :. :.\* : \* :. :.\* : \*

HBO1 GKKNKIYQNLCLLAKFLDHLKTLTYDVEPFLFYVMTADNTGCHLIGYFSKEKNSFLNY  
yEsa1 GRKQRTWCRNLCLLSKFLDHLKTLTYDVPFLFYCMTRRDELGHHLVGYSKEKESADGY  
\*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*

HBO1 NVSCILTMPQYMRQGYGKMLIDFSYLLSKVEEKVGSPERPLSDGLISRSYWKEVLLRY  
yEsa1 NVACILTLQPQYQRMGYGKLLIEFSYELSKKENKVGSPKPLSDGLLSYRAYWSDTLITL  
315 327 338  
\*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*

HBO1 LHNFGKEISKEISQETAVNPVDIVSTLQALQMLKYWKGHVLVKRQDLIDEWIAKEAK  
yEsa1 LVEHQ-KEITIDEISSMTSMTTDLHTAKTLNLRYYKGQHIIFLNEDILDYRNRLKAK  
\*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*

HBO1 RSNSNKTMDPCLKWTPPKGT-----  
yEsa1 K---RRITDPNRLIWKPPVFTASQLRFAW  
: . :.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*.\*.\*.\*.\* : \*

○ Mutation site

FIGURE 72

# Dominant Negative Mutants for PIM-1

Point mutant : K67A, D186N - D186N is a mutation in the activation loop of the kinase domain. (Mol Gen Genet. 1997 May 20;254(5):562-70.PMID: 9197416)

```

*->yelleklGeGsfGkVykakhkdkgtkiVAVKilkkekesikek....
      Y+++ 1G+G+fg+Vy ++++ +++ +VA+K + k +i+++++ +
PIM1 38 YQVGPLLGGGFGSVYSGIRV-SDNLPVAIKHVE--KDRISDWgelp 81
      rflrEiqilkrLs..HpNIvrligvfedtdhlylvmEymegG.dLf
      +++r+ +E+ +lk+++s++ +rll++++fe ++d++ l++E e +dLf
PIM1 82 ngtrVPMEVVLKKVSSGFGSVIRLLDWE-RPDSFVLILERPEPVqDLF 130
      dylrrngplsekeakialQilrGleYlHsngivHRDLKpeNILldend
      d+++++g +l e+ a+++++Q+l+++ ++H++g++HRD+K eNIL+d n+
PIM1 131 DFITERG-ALQEEIARsFFWQVLEAVRHCHNCGVLHRDIKDENILIDLNR 179
      gtvKiaDFGLArlllessklttfvGTpwYmmAPEvileg.rgysskvDvW
      g +K++DFG +ll+ ++ +t+f GT++Y +PE+ +++++r++++ + vW
PIM1 180 GELKLIDFGSGALLK-DTVYTFDGTGRVYS-PPew-IRYhRYHGRSAAVW 226
      SlGvilyelltgglfpagadlpafggdevdqliifvklpfdselpktr
      SlG++Ly +++g
PIM1 227 SLGILLYDMVCG-----DIPFEH----- 244
      idpleelfriikrpglrlplpsncseelkdLlkkcLnkDpskRpGsatak
      ee+ r++ + +++S+e+++L+++CL++ Ps+Rp t++
PIM1 245 ---DEEIIIRGQVF-----FRQRVSSECQHLIRWCLALRPSDRP---TFE 282
      eilnhpwf<-*
      ei nhpw+
PIM1 283 EIQNHPWM 290
      O Mutation site

```

FIGURE 73

# No Significant Antiproliferative Effect is Observed With GFP-NKIAMRE Dominant Negative Mutants in Either A549 or H1299 Cells

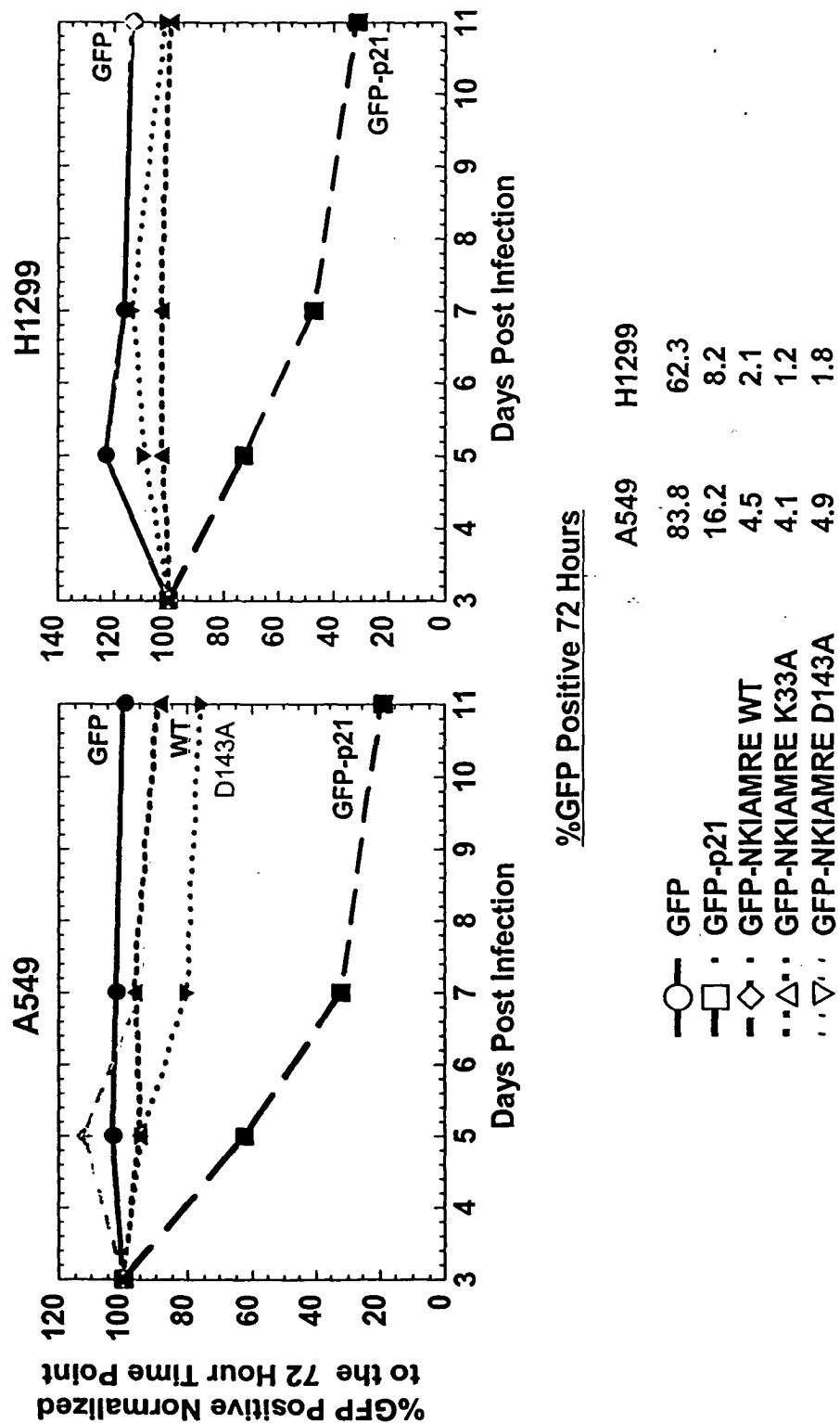


FIGURE 74